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September 27, 2004, 19:19:42; Search time 120 Seconds (without alignments) 1254.185 Million cell updates/sec
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                                                                                                                                                                                                                                      1 MTPEDPEETQPLLGPPGGSA......CVPETKGKTLEQITAHFEGR 477
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                          1017041 seqs, 315518202 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                             OM protein - protein search, using sw model
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sp bacteria:*
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Perfect score:
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Description	Q8wuz9 homo sapien Q7zwh3 brachydanio	Q8ayp6 gallus gall Q8vdj4 mus musculu	Q8wz05 homo sapien	Quepsi ovis aries	Ognera mus muscuiu	Q8mkk4 drosophila	Q86p59 drosophila	Q9v609 drosophila	Q9v608 drosophila	09vu17 drosophila	O8iqh6 drosophila	Ogv610 drosophila	Q93yp9 arabidopsis
SUMMARIES	Q8WUZ9 Q7ZWH3	Q8AYP6 Q8VDJ4	Q8WZ05	Q8SPS1	OSBINZ	QBMCC2 QBMKK4	Q86P59	609A60	809A6O	Q9VU17	0810н6	Q9V610	Q93YP9
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% Query Match Length DB	477	482	248	246	497	443	506	489	857	539	471	433	488
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Score	2457 1411.5	1407	1131	1125.5	946	804.5	789.5	788.5	788.5	788	787	764.5	736
Result No.	2 1	w 4	5	9	7	ao on	10	11	12	13	14	15	16

Q9frl3 arabidopsis		Q9ln48 arabidopsis	Q9xhw3 oryza sativ	Q39416 beta vulgar	Q8t0t6 drosophila	Q8vzi5 arabidopsis	Q8lbi9 arabidopsis	Q8lfr8 arabidopsis	Q9v3g0 drosophila	Q9zu87 arabidopsis	Q9maa4 arabidopsis	Q9leg2 lycopersico	Q9vnj2 drosophila			07xiz0 oryza sativ		O83qb4 shigella fl			_				Q8vzr6 arabidopsis			022848 arabidopsis
Q9FRL3	Q9V848	O9LN48	Q9XHW3	039416	QSTOT6	Q8VZIS	Q8LBI9	QBLFR8	Q9V3G0	Q9ZU87	Q9MAA4	Q9LEG2	Q9VNJ2	Q8Z401	Q8ZMA0	07XIZ0	Q7UBR3	Q83QB4	Q8FE99	012680	Q83EH4	Q7UBN5	O8XCW7	083092	Q8VZR6	065799	OBXEV6	022848
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29.9	29.6	29.5	29.4	29.4	28.9	27.8	27.5	27.3	27.1	26.9	26.6	26.5	26.3	24.7	24.7	24.6	24.5	24.5	24.5	24.2	24.2	23.9	23.9	23.9	23.8	23.8	23.7	23.7
734	727	724.5	723	722	710.5	684	675	670	666.5	662	653.5	650.5	647	607	607	604.5	603	603	601	594.5	593,5	587.5	587.5	587.5	585	584.5	583.5	582
17	. 65 1 rd	91	200	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	96	37	38	9.6	4	4	4.2	43	44	45

## ALIGNMENTS

Strausberg R.;
Strausberg R.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.

- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
- SIMILARITY: BELONGS TO THE SUGAR TRANSPORTER FAMILY.

EMBL; BC019043; AAH19043.1.7.

EMBL; BC019043; AAH19043.1.7.

EMBL; BC019043; AAH19043.1.7.

GO; GO:0016021; F:sugar porter activity; IEA.

GO; GO:0005215; F:transporter activity; IEA.

GO; GO:000863; P:sugar porter activity; IEA.

InterPro; IPR00714; MFS.

InterPro; IPR00714; MFS.

InterPro; IPR005828; Sug\_transporter.

InterPro; IPR005829; Sug\_transporter.

InterPro; IPR005829; Sug\_transporter.

InterPro; IPR005829; Sug\_transporter.

INTERPROSITE; PR0011; SUGAR\_TRANSPORT.

ITGREAMS; TIGR0087; SP; 1.

DR PROSITE; PS00217; SUGAR\_TRANSPORT\_2; 1.

PROSITE; PS00217; SUGAR\_TRANSPORT\_2; 1.

R HYDOLHOELICAI protein; SUGAR\_TRANSPORT; Transmembrane; Transport.

SEQUENCE 477 AA; 50819 MW; 0B480F94AF063316 CRC64; Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI\_TaxID=9606; 100.0%; Score 2457; DB 4; Length 477; 100.0%; Pred. No. 2.4e-157; Ol-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
Homo sapiens (Human). 477 AA PRT; PRELIMINARY; Query Match Best Local Similarity SEQUENCE FROM N.A. TISSUE=Skin; Q8WUZ9 RESULT 1 28WUZ9 SON DE PARTE DE PARTE

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Mismatches
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                  63;
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01-MAR-2003 (TrEMBLrel. 23, La
01-CCT-2003 (TrEMBLrel. 25, La
Glucose transporter type 8.
                Conservative
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QAGFKG 494
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                282;
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                                         MTPEDPEETQPLIGPPGGSAPRGRRVFLAAFAAALGPLSFGFALGYSSPAIPSLQRAAPP
                                                                         MTPEDPEETQPLGPPGGSAPRGRRVFLAAFAALGPLSFGFALGYSSPAIPSLQRAAPP
                                                                                                                    61 APRLDDAAASWFGAVVTLGAAAGGVLGGWLVDRAGRKLSLLLCSVPFVAGFAVITAAQDV
                                                                                                                                                                                                    WMLLGGRLLTGLACGVASLVAPVYISEIAYPAVRGLLGSCVQLMVVVGILLAYLAGWVLE
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            Gaps
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-GTT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
Brachydanio rerio (Zebrafish) (Danio rerio).
Bukaryota, Metazoa; Chordata; Craniata; Verrebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; NCBI TaxID=7955;
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      0; Mismatches
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PROSITE; PS00216; SUGAR_TRANSPORT_1; 2.
PROSITE; PS00217; SUGAR_TRANSPORT_2; 1.
    Conservative
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RA SECURACE FROM N.A.

RA GLOCOSE transporter 8 plays a major role in insulin-responsive
ET "Glocose transporter in place of glucose transporter 4 in chickens.";
ET glucose transporter in place of glucose transporter 4 in chickens.";
ET glucose transporter in place of glucose transporter 4 in chickens.";
ET glucose transporter in place of glucose transporter 4 in chickens.";
ET glucose transporter in place of glucose transporter 4 in chickens.";
ET glucose transporter 5 c. the membrane; EA.

ET glucose transporter 6 c. the membrane; EA.

ET glucose transporter 6 c. the membrane; EA.

ET glucose transporter 6 c. the chickens.";

ET glucose transporter 7 c. the chickens.";

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                                               TPEDPEETQPLLGPPGGSAPRGRRVFLAAFAAALGPLSFGFALGYSSPAIPSLQRAAPPA
                                                                                           17 TEEDRSEQDAYL-----DKVKNGKLFIATFAAVLGPLSFGFVLGYSSPAIPELRRIQDLR
                                                                                                                                                                       62 PRLDDAAAASWFGAVVTLGAAAGGVLGGWLVDRAGRKLSLLLCSVPFVAGFAVITAAQDVW
                                                                                                                                                                                                          122 MLLGGRLLIGLACGVASLVAPVYISEIAYPAVRGLLGSCVQLMVVVGILLAYLAGWVLEW
                                                                                                                                                                                                                                                                                                                                        132 MFYVGRVLTGLASGVTSLVVPLYISEMAHERVRGTLGSCVQLMVVIGIMGAYVTGLFLDW
                                                                                                                                                                                                                                                                                                                                                                                                              182 RWLAVLGCVPPSLMLLLMCFMPETPRFLLTQHRRQEAMAALRFLWGSE--QGW----ED
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      Gaps
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Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
Gallus.
   19;
   Indels
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Last annotation update)
122;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     359 VSAQPVDASVGLAWLAVGSMCLFIAGFAVGWGPIPWLLMSEIFPLHVKGVATGICVLTNW 418
                                                                                                                                                                                                                                                                                                                                                               123
                                                                                                                                                                                                                                                                                                                                                                                                                                 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   124 LGGRLLTGLACGVASLVAPVYISEIAYPAVRGLLGSCVQLMVVVGILLAYLAGWVLEWRW 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         240 -EQSFHLALLRQPGIYKPFIIGVSLMAFQQLSGVNAVMFYAETIFEEAKFKDSSLASVVV 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GVIQVLFTAVAALIMDRAGRRLLLLVLSGVVNVFSTSAFGAYFKLTQGGPGNSSHVAISAP 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63
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                                                                                                                                                                                                                                                                                                                                                               LDDAAASWFGAVVTLGAAAGGVLGGWLVDRAGRKLSLLLCSVPFVAGFAVITAAQDVWML
                                                                                                                                                                                                                                                                                                                                                                                                  419 LMAFLVTKEFSSLMEVLRPYGAFWLASAFCIFSVLFTLFCVPETKGKTLEQITAHF 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        424 WMAFLVIKEFHDFIGFLISYGTFWLFSAFCCLSVTFAAFYVPETKGRTLEQIEAYF 479
                                                                                                                                                                                                                                                                                LAVLGCVPPSLMLLIMCFMPETPRFLLTQHRRQBAMAALRFLWGS--EQGWEDPP1GA--
                                                                                                                                                                                                                                   EETQPILGPPGGSA---PRGRRVFLAAFAALGPLSFGFALGYSSPAIPSLQRAAPPAPR
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R GO; GO:0016021; C:integral to membrane; IEA.

R GO; GO:0005215; F:transporter activity; IEA.

GO; GO:0005215; F:transporter activity; IEA.

GO; GO:0006643; P:carbsporter activity; IEA.

R GO; GO:0006643; P:carbsporter activity; IEA.

R InterPro; IPR007114; MFS.

R InterPro; IPR005828; Sub_transporter.

R InterPro; IPR005829; Sug_transporter.

P Fram; PR00171; Sugar_transporter.

R PR01712; PR00171; Sugar_transporter.

R PR01712; PR00171; Sugar_transporter.

R PR0517E; PS00850; MES; 1.

R PR0517E; PS00216; Sugar_transporter.

R PR0517E; PS00216; Sugar_transport; Transmembrane; Transport.

T NON_TER
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Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY)
-!- SIMILARITY: BELONGS TO THE SUGAR TRANSPORTER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                     8;
                                                                                                       DB 13; Length 482;
                                                                                                                                                                         Indels
      SUGAR TRANSPORT 2; 1. 53349 MW; CCFD0CA15F44C976 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-WAR-2002 (TrEMBLrel. 20, Created)
01-WAR-2002 (TrEMBLrel. 20, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                    57.3%; Score 1407; DB 13;
59.2%; Pred. No. 9.5e-87;
iive 68; Mismatches 118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               266
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical protein (Fragment). Mus musculus (Mouse).
                                                                                                                                          Local Similarity 5.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                            482 AA;
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             PS00217;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               299
             PROSITE;
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                             64
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                                                                                                          Query Match
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OGNUDA
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                                                                                             3
                                                                                                                                                                                                                                                                                                                                     FSTSAFGAYFKLTQGGPGNSSHVAISAPVSAQPVDASVGLAWLAVGSMCLFIAGFAVGWG 390
                                                                                                                                                                                                                                                                                                                                                                                                                                  PIPWLLMSEIFPLHVKGVATGICVLTNWLMAFLVTKEFSSLMEVLRPYGAFWLASAFCIF 450
                                                                                                                                                                                                                                                                                                                                                                     180 PIPWLLMSEIFPLHVKGVATGVCVLTNWFWAFLVTKEFSSVMBMLRPYGAFWLTAAFCAL 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
                                                                                                                                          270
                                                                                                                                                                                                                                       271 GVNAVMFYAETIFEEAKFKDSSLASVVVGVIQVLFTAVAALIMDRAGRRLLLVLSGVVMV 330
                                                                                                                                                                                                                                                                                          120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              164 MYVYGILLAYLAGWYLEWRWLAYLGCYPPSLMLLLMCFMPETPRFLLTQHRRQEAWAALR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MVVGILLAYLAGWVLEWRMLAVLGCVPPSLMLLLMCFMPETPRFLLTQHRQEAMAALR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              224 FLWGSEQGWEDPPIGAEQSFHLALLRQPGIYKPFIIGVSLMAFQQLSGVNAVMFYAETIF
                                                                                                                                          212 QHRRQEAMAALRFLWGSEQGWEDPPIGAE-QSFHLALLRQPGIYKPFIIGVSLMAFQQLS
                                                                                                                                                                      1 QHQYQBAMAALRFLWGSEEGWEEPPVGAEHQGFQLALLRRPGIYKPLIIGISLMVFQQLS
                                                                                                                                                                                                                                                                             61 GVNAIMFYANSIFEEAKFKDSSLASVTVGIIQVLFTAVAALIMDRAGRRLLALSGVIMV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
Bakaryota: Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Thang P.P., Zhou X.M., Jiang H.Q., Huang Y., Qin W.X., Zhao Wan D.F., Gu J.R., "Novel human cDNA clones with function of inhibiting cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              growth."; submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases. submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases. SUBMITTED REGELLIAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY 8 EMBL, AF289587; AAL55771.1; -
GO; GO:0005215; Cintegral to membrane; IEA.
GO; GO:0005215; Firtansporter activity; IEA.
InterPro; IPR007114; MFS.
                                             47.5%; Score 1167; DB 11; Length ilarity 83.1%; Pred. No. 6.9e-71; Conservative 20; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27017 MW; AA929A749BBEE558 CRC64;
29132 MW; 1B3031928863B0FC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
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llarity 93.0%; Pred. No. 1.7e-68;
Conservative 5; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS50850; MFS; 1.
PROSITE; PS00216; SUGAR TRANSPORT_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Interpro; IPR005828; Sub_transporter.
InterPro; IPR005829; Sug_transporter.
Pfam; PF00083; sugar_tr; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         451 SVLFTLFCVPETKGKTLEQITAHFEGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein; Transmembrane
SEQUENCE 248 AA; 27017 MW; AA922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-2002 (TrEMBLrel. 20, 01-MAR-2002 (TrEMBLrel. 20, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical protein.
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          266 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
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Query Match
Best Local Similarity 43.64
Matches 214; Conservative
                                                                                          PRELIMINARY;
                                                                                                                                                                                                                      Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                          NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           59
                                                   RESULT 7
                                                                                                         ACCOORDING TO THE STATE OF THE 
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QGGPGNSSHVAISAPVSAQPVDASVGLAWLAVGSMCLFIAGFAVGWGP-IPWLLMSEIFP 402
                                                                            219 MAALRFLWGSEQGWEDPPIGAE-QSFHLALLRQPGIYKFFIIGVSLMAFQQLSGVNAVMF 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     337
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        278 YAETIFEEAKFKDSSLASVVVGVIQVLFTAVAALIMDRAGRRLLLVLSGVVMVFSTSAFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AYFKLTQGGPGNSSHVAISAPVSAQPVDASVGLAWLAVGSMCLFIAGFAVGWGPIPWLLM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEIFPLHVKGVATGICVLTNWLMAFLVTKEFSSLMEVLRPYGAFWLASAFCIFSVLFTLF
                                                                                                                                                                                                                                                                                                                                                                               Vuls aries (Sheep).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea
Boyidae, Caprinae, Ovis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Limesand S.W., Regnault T.R.H., Hay W.W. Jr., "Characterization of Glucose Transporter 8 (GLUT8) in the Ovine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            45.8%; Score 1125.5; DB 6; Length 246; 88.2%; Pred. No. 3.9e-68; ive 11; Mismatches 17; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26537 MW; E8F3871946CD0723 CRC64;
                                                                                                                                                                                                                                                                                             01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Glucose transporter 8 (Fragment)
                                                                                                                                                                                                                                                                  246 AA
                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 217; Conservative
                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        246 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CVPETK 246
                                                                                                                                                                                                                                                                                                                                                                         Ovis aries (Sheep)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                    LHLQ 239
                                                                                                                                LHVK 406
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PPAPRLDDAAASWFGAVVTLGAAAGGVLGGWLVDRAGRKLSLLLCSVPFVAGFAVITAAQ 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         179 LEWRWLAVLGCVPPSLMLLLMCFMPETPRFLLTQHRRQEAMAALRFLWG-SEQGWEDPPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     238 G---AEQSFHL--ALLRQPGIYKPFIIGVSLMAFQQLSGVNAVMFYABTIFEEAK-FKDS
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                                                                                                   Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Similar to solute carrier family 2.
F630103L12RIK.
497 AA
PRT;
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Oy 284 EEAKFKDSSLASVVVGVIQVLFTAVAALIM		USWAKK4 PRELIMINARY, PRT; 488 AA AC QBWKK4; DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence un DT 01-OCT-2003 (TrEMBLrel. 22, Last sequence un DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence un DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation DE AT19440p (CG8234-PA). GN AT19440p (CG8234-PA). GN BURATYOTA; Metazoa; Arthropoda; Hexapoda; IOC Bukaryota; Metazoa; Arthropoda; Hexapoda; IOC Neoptera; Endopterygota; Diptera; Brachycer OC Rehydroidea; Drosophiladae; Drosophila.	OX NCBI_TaxID=7227;  RN 5101 RP Stableton M., Brokstein P., Hong L., Agbaya RA Champe M., Chavez C., Dorsett V., Dresnek D RA George R., Gonzalez M., Guarin H., Kromill RA Miranda A., Mungall C.J., Nunco J., Pacleb RA Celniker S.; RL Submitted (JUN-2002) to the EMBL/GenBank/DD RR SEOURNCE FROM N.A. STEDINE BETKELEY; RA MEDLINE=20196006; PubMed=10731132; RA Adams M.D., Celniker S.E., Holt R.A., Evans RA Adams M.D., Celniker S.E., Holt R.A., Evans RA George R.A., Lewis S.E., Richards S., Babbu	RA Brandon R.C., Rogers YH.C., Blazej R.G., RA Wan K.H., Doyle C., Baxter E.G., Helt G., N RA Abril J.F., Agbayani A., An HJ., Andrews-RA Ballew W.M. Basu A., Baxendale J., Bayrakt RA Benson K.Y., Benos P.V., Berman B.P., Bhand RA Borkova D. Botchan M.R., Bouck J. Barokate RA Burtis K.C., Busam D.A., Butler H., Cadieu RA Gerlos B., Delcher A., Deng Z., Mays A.D Gerlos B., Delcher A., Deng Z., Mays A.D Dodson K., Doup L.E., Downes M., Dugan-Roch RA Durbin K.J. Evangelista C.C., Ferraz C., F RA Durbin K.J., Evangelista C.C., Ferraz C., F RA Glodek A., Gong F., Gorrell J.H., Gu Z., Gulb RA Harris N.L., Harrey D., Heiman T.J., Hernan RA Hostin D., Houston K.A., Howland T.J., Hernan RA Hostin D., Houston K.A., Howland T.J., Wei Lasko P., Lei Y., Levitsky A.A., Li J., Li RA Liu X., Mattei B., McIntosh T.C., Molecod M. RA Molson K.A., Mixphy L., Mrsket RA Dalazzolo M., Pittman G.S., Pan S., Pollard RA Rainert K., Remington K., Saunders R.D.C.,
407 GVATGICVLTNWLMAPLVTKEFSSLMEVLRPYGAFWLASAFCIFSVLFTLFCVPETKGKT 466 421 GVASGLCVLVSWLTAFVLTNYFLLAVNAFGLQVPFFFFSAICLLSLLFTGCCVPETKGRS 480 467 LEQITAHFEGR 477 481 LEQIEAFFHTR 491	NCC2 OBNCC2 OBNCC2 O1-CCT-2002 (TEEMBLES 22, CZ 01-CCT-2002 (TEEMBLES 22, LA 01-CCT-2003 (TEEMBLES 22, LA 01-CT-2003 (TEEMBLES 22, LA 01-CT-2003 (TEEMBLES 22, LA 01-CT-2003 (TEEMBLES 22, LA	DENGATYOLD, METAZOA; CHORDATA; CRAINATA; VERTEDRATA; EUREleoSCOMI;  OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  OX NCBI TAXID=9606;  RN [1]  RP SEQUENCE FROM N.A.  RA ISOGAI T., Ota T., Nishikawa T., Hayashi K., Otsuki T., Sugiyama T.,  RA SUZUKi Y., Nagai K., Sugano S., Ishii S., Kawai-Hio Y., Saito K.,  RA Mamanoto O., Wakamatsu A., Nakamura Y., Kojima S., Nagahari K.,  RA Masuho Y., Ono T., Okano K., Yoshikawa Y., Actsuka S., Sasaki N.,  RA Hattori A., Okumura K., Iwayanagi T., Ninomiya K.;  RT "MEDO human CNNA Sequenching project.";  RT, Shipmitted (MAR-2002) to the EMBL/Genbank DDBJ databases.	CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).  C1 -!- SIMILARITY: BELONGS TO THE SUGAR TRANSPORTER FAMILY.  DR G0; G0: 0005321; F: BELONGS TO THE SUGAR TRANSPORTER FAMILY.  DR G0; G0: 0005321; F: sugar porter activity; IEA.  G0; G0: 0005321; F: sugar porter activity; IEA.  DR G0; G0: 0005321; F: transporter activity; IEA.  DR G0; G0: 0005431; P: carbohydrate transport; IEA.  DR InterPro; IPR00363; Sugar transporter.  DR InterPro; IPR00363; Sugar transporter.  DR RINTS; PR00171; SUGARTRNSPORT.  DR PROSITE; PS00816; SUGAR_TRANSPORT_1; 1.  DR PROSITE; PS00816; SUGAR_TRANSPORT_1; 1.  KW Hypothetical protein; Sugar transmort; Transmembrane; Transport.  KW Hypothetical protein; Sugar transport; Transmembrane; Transport.	Aar Aar

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TLAVGSMCLFIAGFAVGWGPIPWLLMSE 399
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                                                                                                                                                                  EVLRPYGAFWLASAFCIFSVLFTLFCV 459
MDRAGRRILLVLSGVVMVFSTSAFGAY 339
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Hoskins R.A., Galle R.F.,
Shourner M., Henderson S.N.,
Zhang Q., Chen L.X.,
G., Champe M., Pfeiffer B.D.,
G., Champe M., Pfeiffer B.D.,
G., Chambor C.R., Miklos G.L.G.,
ews-Pfannkoch C., Baldwin D.,
raktaroglu L., Beasley E.M.,
kstein P., Brottier P.,
ieu B., Center A., Chandra I.,
nport L.B., Davies P.,
A.D., Dew I., Dietz S.M.,
Rocha S., Dunkov B.C., Dunn P.,
Ferriera S., Fleischmann W.,
Guan P., Harris M.,
Guan P., Harris M.,
rnandez J.R., Houck J.,
wei M.-, Ibeqwam C.,
wei M.-, Ibeqwam C.,
ti Z., Kulp D., Lai Z.,
ti Z., Kulp D., Lai Z.,
d M.P., McPherson D.,
Morris J., Moshrefi A.,
Morris J., Moshrefi A.,
Muzny D.M., Nelson D.L.,
skern D.R., Pacleb J.M.,
lard J., Puri V., Reese M.G.,
C., Scheeler F., Shen H.,
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k D., Farfan D., Frise E.,
iller B., Li P., Liao G.,
eb J., Paragas V., Park S.,
., Lewis S.E., Rubin G.M.,
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|MDLAGRKVL------
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era; Muscomorpha;
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Celniker S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,

Beans C.A., Gacayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,

Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,

Ratlson J.W., Center A., Champe M., Davenport L.B., Dietz S.W.,

Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.W.,

A Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.W.,

R. Perriera S., Frise E., Galle R.F., Garg N.S., George K.A.,

A Perriera M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,

A McIntosh T.C., Moy M., Murphy B.A., Nelson C., Malson K.A., Nunco J.,

R. Poudanenavong S., Pittman G.S., Parel S., Pétifer B.,

Rabele J., Paragas V., Park S., Parel S., Pétifer B.,

Rabele J., Rirong R., Svirskas R., Tector C., Tyler D.,

Milliams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.,

"Sequencing of Drosophila melanogaster genome.",

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-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY)
-!- SIMILARITY: BELONGS TO THE SUGAR TRANSPORTER FAMILY.
EMBL, AX122079; AAM52591.1; -.
EMBL, AE003825; AAM68715.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mista S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell Hardecky P., Hung Y., Kaminker J.S., Prochnik S.E., Smith C.D., Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E., Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N. Krommiller B., Marshall B., Millburn G., Richter J., Russo S., Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E., Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E., Mannotation of Drosophila melanogaster genome.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                S.E., Gibbs R.A., Rubin G.M., Venter C.J., to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PlyBase; FBGT0033644; CG8234.
GO; CO:0016021; C:integral to membrane; IEA.
GO; GO:0005351; F:stagar porter activity; IEA.
GO; GO:0005215; F:transporter activity; IEA.
GO; GO:0006515; F:transporter activity; IEA.
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PROSITE; PS00216; SUGAR_TRANSPORT_1; 2.
PROSITE; PS00217; SUGAR_TRANSPORT_2; 1.
Sugar_transport; Transmembrane; Transport
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InterPro, IPR005829; Sug_transpt.
Pfam, PF00083; Sugar tr; 1.
PRINTS; PR00171; SUGATRNSPORT.
TIGREAMS; TIGR00879; SP; 1.
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Submitted (MAR-2000)
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GWLVDRAGRKLSLLLCSVPFVAGFAVITAAQDVWMLLGGRLLIGLACGVASLVAPVYISE
                                                                                                            TLQPEVRGTLGLLPTALGNIGILVCYVAGSFMNWSMLAFLGAALPVPFLILMIIIPETPR
                                                                                                                                                          269 LSISLGLMFFQQFSGINAVIFYTVQIFKDAGSTIDSNLSTIVGVVNFFATFMGIILIDR
                                                                                         148 IAYPAVRGLLGSCVQLMVVVGILLAYLAGWVLEWRWLAVLGCVPPSLMLLLMCFMPETPR
                                                                                                                                           FLLTQHRRQEAMAALRFLWGSE------QGWEDPPIGAEQSFHLALLRQPGIYKP
                                                                                                                                                                                           FIIGUSLMAFQQLSGVNAVMFYAETIFEEA-KFKDSSLASVVVGVIQVLFTAVAALIMDR
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Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,
Miranda A., Mungall C.G., Nunco J., Pacleb J., Paragas V., Park S.,
Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota, Neopeta, Endopterygota, Diptera, Brachycera, Muscomorpha, Ephydroidea, Drosophilidae, Drosophila.
                                                                                                                                                                                                                                                            329 LGRKILLYVSDIAMIVTLSILGGFFYCKAHGP-DVSH------
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PROSITE; PS00216; SUGAR TRANSPORT 1; 2.
PROSITE; PS00217; SUGAR TRANSPORT 2; 1.
SEQUENCE 506 AA; 55235 MW; 24E8718260D4319B CRC64;
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Last sequence update)
Last annotation update)
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Celniker S.;
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Similarity

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Query Match

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RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amaratides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Amaratides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Roman B.P., Zhang Q., Chen L.X.,
RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Baxendale J., Bayraktaroglu L., Bassley E.M.,
RA Beson K.Y., Berman B.P., Bhandari D., Bottier P.,
RA Borkova D., Botchan M.R., Bouck J., Brokatein P., Brottier P.,
RA Cherry J.M., Cawley S., Dahlke C., Davengort L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davengort L.B., Davies P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Fosler C., Gabriellan A.B., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        447
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                                                                                                                                                                                            LAALSVSLGSLVVGFVSAYTSPALVSMTDRNITSFEVTQDAGSWVGGIMPLAGLAGGIAG
                                                                                                                                                                                                                                                                                                               TVQPEVRĞTLĞLLPTAFGNIĞILLCFVAĞSFMNWSMLAFLĞAALPVPFLILMFLIPETPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   388 TCFVIYILGFSLGFGPIPWLMMGELLPAKIRGSAASVATAFNWFCTFVVTKTFQDLTVAM
                                                                                                                                    28 LAAFAAALGPLSFGFALGYSSPAIPSLQRAAPPAPRLDDAAASWFGAVVTLGAAAGGVLG
                                                                                                                                                                                                                                                                     GWLVDRAGRKLSLLLCSVPFVAGFAVITAAQDVWMLLGGRLLTGLACGVASLVAPVYISE
                                                                                                                                                                                                                                                                                                                                                                                                      148 IAYPAVRGLLGSCVQLMVVVGILLAYLAGWVLEWRWLAVLGCVPPSLMLLLMCFMPETPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FLLTQHRRQEAMAALRFLWGSEQGWE------DPPIGAEQSFHLALLRQPGIYKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WFVGRGLEERARKALKWLRGKEADVEPELKGLMRSQADADRQASRNTMLELLKLNNL-KP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FIIGVSLMAFQQLSGVNAVMFYAETIFEEA-KFKDSSLASVVVGVIQVLFTAVAALIMDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                346 AGRKILLYVSDIAMVLTLFVLGGFFYCKTYGP-DVSH------LGWLPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               376 GSMCLFIAGFAVGWGPIPWLLMSEIFPLHVKGVATGICVLTNWLMAFLVTKEFSSLMEVL
                                                                     Gaps
                                                                         31;
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                                                                         Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   436 RPYGAFWLASAFCIFSVLFTLFCVPETKGKTLEQITAHFEGR
Score 789.5; DB 5;
Pred. No. 3.3e-45;
75; Mismatches 183;
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NCBI_TaxID=7227;
      32.18;
                                                                     173; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                  Similarity
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                                                                                                                                                                                                                                                                     88
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   Query Match
Best Local 8
                                                                  Matches
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Q9V609
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A Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C., Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Kalumel B.E., Kodirac C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., R.A. Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D., R.A. McKulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A., A. Merkulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A., R. Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L., R.A. Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., R.A. Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H., R.A. Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., Spier E., Stradling A.C., Stapleton M., Strong R., Sun E., Spradling A.C., Stapleton M., Strong R., Sun E., Spradling A.C., Stapleton M., Strong R., Sun E., Mang Z.-Y., Wassarman D.A., Weinstcock G.M., Weissenbach J., Wang X., Milliams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., R.A. Zheng X.H., Zhong F.W., Zhong W., Zhuo S., Zhuo X., Smith H.O., R.A. Zheng X.H., Zhong F.W., Zhous W., Zhuo S., Zhuo X., Smith H.O., R. The genome sequence of Drosophila melanogaster.", Science 287:2185-2195 (2000).

Els Sullear R. Sullear R. Sheng X. R. Shirk R. Science 287:2185-2195 (2000).

Els Sullear R. Sheng X. R. Shirk R. Sh
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       371 TCFVIXILGFSLGFGPIPWLMMGEILPAKIRGSAASVATAFNWFCTFVVTKTFQDLTVAM 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          316 AGRRILLLVLSGVVMVFSTSAFGAYFKLTQGGPGNSSHVAISAPVSAQPVDASVGLAWLAV 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GSMCLFIAGFAVGWGPIPWLLMSEIFPLHVKGVATGICVLTNWLMAFLVTKEFSSLMEVL 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          148 IAYPAVRGLLGSCVQLMVVVGILLAYLAGWVLEWRWLAVIGCVPPSLMLLLMCFMPETPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               208 FILTQHRRQEAMAALRFLWGSEQGWE-----DPPIGAEQSFHLALLRQPGIYKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               257 FIIGVSLMAFQQLSGVNAVMFYAETIFEEA-KFKDSSLASVVVGVIQVLFTAVAALIMDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       269 LSISLGLMFFQQFSGINAVIFYTVQIFKDAGSTIDGNLCTIIVGIVNFLATFIGIVLIDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28 LAAFAAALGPLSFGFALGYSSPAIPSLQRAAPPAPRLDDAAASWFGAVVTLGAAAGGVLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TIGKFANS; 11GNOVOLONG, PROSTED; PROSTED; PSSOBSO, MFS; 1.
PROSITE; PSGO216; SUGAR_TRANSPORT_1; 2.
PROSITE; PSGO217; SUGAR_TRANSPORT_2; 1.
SUGAR_transport; Transmembrane; Transport.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches 183;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   32.1%; Score 788.5; DB 5
37.2%; Pred. No. 3.7e-45;
ive 76; Mismatches 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AE003825; AAF58631.1; -.
FlyBase; FBgn0050035; CG30035.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0005351; F:sugar porter activity; IEA.
GO; GO:0005215; F:transporter activity; IEA.
GO; GO:000643; P:carbohydrate transport; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR007114; MFS.
InterPro; IPR005828; Sub_transporter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR003663; Sugar transpt.
InterPro; IPR008629; Sug transporter.
Pfam: PF00083; Sugar tr. 1.
PRINTS; PR00171; SUGRIRNSPORT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TIGR00879; SP; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., Barantides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., Button G.G., Worthern J.R., Yandell M.D., Zhang Q., Chen L.X., Button G.G., Worthan J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Fefeifer B.D., RA Brandon R.C., Bayer E.G., Helt G., Nolson C.R., Miklos G.L.G., Randon R.C., Bayer E.G., Champe M., Fefeifer B.D., RA Ballew R.M., Basu A., Baxendall G., Bayrakaracollu L., Beasley E.M., Ballew R.M., Basu A., Baxendall G., Bayrakaracollu L., Beldrain D., RA Ballew R.M., Baren B.D., Buttler H., Cadieu E., Center A., Chandra I., Rokova D., Buttler H., Cadieu E., Center A., Chandra I., Ra Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., Cherry J.M., Cawley S., Dahlke C., Perraz C., Ferraz C., Ferraz C., Ferraz C., Ferraz C., Ra Goog K., Doug L.B., Downson M., Bugan-Rocha S., Dunkov B.C., Dunn P., Botter M., Baris M.L., Harvey D., Heiman T.J., Herrien S., Chelter A., Goog F., Gorrell J.H., Gu Z., Guan P., Harris M., A., Kalush F., Karpen G.H., Wei M.-H., Ibegwam C., Alasko P., Lei Y., Harvey D., Heiman T.J., Hernandez J.R., Harris M., A., Kalush F., Karpen G.H., Wei M.-H., Ibegwam C., Laisa G., Mishina N.V., Wobarry C., Morxis J., Moshrefi A., Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D., Merkluov G., Milshina N.V., Ci, M.C., McCaller R., Sander K., Shen H., Rainert K., Pennigton K., Sauders B., Shirk B., Woodar Y. C., Morxis J., Wang A., Shirk B., Shirk 
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Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,
Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,
Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,
Ferriera S., Frise E., Galle R.F., Garg N.S., George R.A.,
Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,
Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,
McIntosh T.C., Moy M., Wurphy B., Nelson C., Nelson K.A., Nunco J.,
Pacleb J., Paragas V., Park S., Patel S., Pfeiffer B., Nunco J.,
                                                                                                                                                                                                                                                                                                                              CG30035 protein.
CG30035 OR CG7797 OR CG7801.
Drosophila melanogaster (Fruit fly)
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha
Ephydroidea, Drosophilidae, Drosophila.
477
                                                    472
                                              431 GAHGAFWLFGAICFVGLFFVIIYVPETQGKTLEDIERKWMGR
436 RPYGAFWLASAFCIFSVLFTLFCVPETKGKTLEQITAHFEGR
                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
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MEDLINE=20196006; PubMed=10731132;
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                                                                                                                                                                                            PRELIMINARY;
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SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ephydroidea; Dros
NCBI_TaxID=7227;
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01-OCT-2003
                                                                                                                                                                                            09V608
                                                                                                                                  RESULT 12
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AGRRILLUVLSGVVMVFSTSAFGAYFKLTQGGPGNSSHVAISAPVSAQPVDASVGLAWLAV 375
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               398 LAALSVSLGSLVVGFVSAYTSPALVSMTDRNITSFEVTQDAGSWVGGIMPLAGLAGGIAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         88 GWLVDRAGRKLSLLLCSVPFVAGFAVITAAQDVWMLLGGRLLTGLACGVASLVAPVYISE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----LGWLPL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---DPPIGAEQSFHLALLRQPGIYKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     257 FIIGVSLMAFQQLSGVNAVMFYAETIFEEA-KFKDSSLASVVVGVIQVLFTAVAALIMDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               458 GPLIEYLGRRNTILATAVPFIVSSLLIACAVNVAMVLCGRFLAGFCVGIASLSLPVYLGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   518 TVQPEVRGTLGLLPTAFGNIGILLCFVAGSFMNWSMLAFLGAALPVPFLILMFLIPETPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               578 WFVGRGLEERARKALKWLRGKBADVEPELKGLMRSQADADRQASRNTMLELLKLNNL-KP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SIMILARITY: BUCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE SUGAR TRANSPORTER FAMILY.
Flybase; PRODUNGSONS. 2; -.
                                                                                                                                                                                                                                           Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D., Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E., Smith C.D., Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E., Kronmiller B., Marshall B., Millburn G., Richter J., Harris N., Kronmiller B., Marshall B., Millburn G., Richter J., Russo S., Searle S.M.J., Smith E., Shu S., Smutniak F., Mhitfield E., Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E., Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
Phouanenavong S., Pittman G.S., Puri V., Richards S., Scheeler F., Stapleton M., Strong R., Svirskas R., Tector C., Tyler D., Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.; "Sequencing of Drosophila melanogaster genome."; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.,
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            857;
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PROSITE; PS00116; SUGAR TRANSPORT 1; 2.
PROSITE; PS00217; SUGAR_TRANSPORT_2; 1.
SUGAR transport; Transmembrane; Transport.
SEQUENCE 857 AA; 95188 WW; 8408E1191B8B7ASF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     76; Mismatches 183;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     32.1%; Score 788.5; DB 5; 37.2%; Pred. No. 6.6e-45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GO, GO:0016021; C:integral to membrane; IBA.
GO; GO:0005351; F:sugar porter activity; IEA.
GO; GO:0002215; F:transporter activity; IEA.
GO; GO:0008643; P:carbohydrate transport; IEA.
InterPro; IPR07114; MFS.
InterPro; IPR05828; Sub_transporter.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR003663; Sugar_transpt.
InterPro; IPR005829; Sug_transporter.
Pfam; PF00083; sugar_tr; 1.
PRINTS; PR00171; SUGRIRNSPORT.
TIGREAMS; TIGR00879; SP; 1.
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                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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Similarity
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01-MAR-2003
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CG10960-PA.
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Matches 178;
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REALINE=2018606; PubMed=10731132;

RADINE=2018606; PubMed=10731132;

RADINESON RADINE RADINE R.G., Mango Q., Chen L.X.,

RADINE RADINE RADINE R.G., Placej R.G., Chango M., Miklos G.L.G.,

RADINE RADINE RADINE R.G., Barman B.R., Malacwas-Feankoch C., Baldwin D.,

RADINE RADINE RADINE R.G., Barman B.P., Bhandari D., Belsinkor B.M.,

RADINE R.D., Botchan M.R., Bouch J.F., Danler R., Canter R., Chandra I.,

RADINE R.G. Busam D.A., Buller H., Cadieu B., Center A., Chandra I.,

RADINE R.G. Busam D.A., Ballke C., Davenport L.B., Davies P.,

RADINE R.G., E., Domes M., Dahlke C., Davenport L.B., Davies P.,

RADINE R.G., E., Domes M., Dahlke C., Davenport L.B., Davies P.,

RADINE R.G., E., Domes M., Dapan-Rocha S., Dunkov B.C.,

RADINE R.G., Rangelista C.C., Ferraz C., Ferraz C., Ferra C., Perra C
                              ::| ||::|:||||| ::| || ::| || 39 TCFVIYILGFSLGFGPIPWLMMGEILPAKIRGSAASVATAFNWFCTFVVTKTFQDLTVAM 798
376 GSMCLFIAGFAVGWGPIPWLLMSEIFPLHVKGVATGICVLTNWLMAFLVTKEFSSLMEVL 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                     436 RPYGAFWLASAFCIFSVLFTLFCVPETKGKTLEQITAHFEGR
                                                                                                                                   Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                          539 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster (Fruit fly).
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CG10960.
                                                                                                                                                                                                                                                                                             PRELIMINARY;
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TGIEAEWATILIGIMQVVATFVSTLVVDKLGRRILLLASGISMAISTTAIGVYFFL---- 410
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   405 VKGVATGICVLTNWLMAFLVTKEFSSLMEVLRPYGAFWLASAFCIFSVLFTLFCVPETKG 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         295 AELRETDRETKANKVNVWAALNRPVTRKALAISMGLMFPQQVCGINAVIFYASRIFLEAN 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PGNSSHVAISAPVSAQPVDAS--VGLAWLAVGSMCLFIAGFAVGWGPIPWLLMSEIFPLH 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    175 AVNVSMLYASRFILGIAGGAFCVTAPMYTGEIAQKEIRGTLGSFFQLMITIGILFVYAVG 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----DPPIGAEQSFHLALLRQPGIYKPFIIGVSLMAFQQLSGVNAVMFYAETIFEEAK 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FK-DSSLASVVVGVIQVLFTAVAALIMDRAGRRLLLIVLSGVVMVFSTSAFGAYFKLTQGG 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      57 AAPPAPRLDDAAASWFGAVVTLGAAAGGVLGGWLVDRAGRKLSLLLCSVPFVAGFAVITA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  177 WVLEWRWLAVLGCVPPSLMLLLMCFWPETPRFLLTQHRROEAMAALRFLWGSEQGWE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
Submitted (jun-2002) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE SUGAR TRANSPORTER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32.1%; Score 788; DB 5; Length 539; 36.2%; Pred. No. 4.4e-45; ive 95; Mismatches 183; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sugar transport; Transmēmbrane; Transport.
SEQUENCE 539 AA; 58413 MW; A2F4814DBF676BBD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                                                    EMBL; AR003540; AAF49874.1; -.
EMBL; AY119564; AAM5218.1; -.
ENDBL; AY119564; AAM5218.1; -.
Elybase; EBR0000316; CG10960.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0005351; F:sugar porter activity; IEA.
GO; GO:0005215; F:transporter activity; IEA.
GO; GO:0008643; P:carbohydrate transport; IEA.
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PROSITE; PS00217; SUGAR_TRANSPORT_2; 1.
                                                                                                                                                                                                                                                                                                                                          InterPro; IPR003663; Sugar_transpt.
InterPro; IPR005829; Sug_transporter.
Pfam; PF00083; sugar_tr; 1.
PRINTS; PR00171; SUGRIRNSPORT.
TIGRPAMS; TIGR00879; SP; 1.
                                                                                                                                                                                                                                                                                      Interpro; IPR007114; MFS.
Interpro; IPR005828; Sub_transporter.
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REGISTRE-20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li F.W., Hoskins R.A., Calle R.E.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Brandon R.C., Rogers Y.H., Blazel R.G., Champe M., Pefeiffer B.D.,
RA Ballew R.M., Basu A., Bazendale G., Melson C.R., Gabor G.L.,
RA Abril J.F., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
RA Ballew R.M., Basu A., Bazendale J., Andrews-Flannach C. B. Baldwin D.,
RA Berson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botcher M.N., Bouck J., Brokstein P., Botchiar P., Botcher R.A,
Borkova D., Botcher A., Deng Z., Mays A.D., Dev I.D., Dev I.D.,
RA Britis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I.,
RA Goson K., Doup L.E., Downes M., Dugar-Rocha S., Dunkov B.C., Dunn P.,
RA Borkova D., Botcher A., Deng Z., Mays A.D., Dev I.D., Dev I., Diet Z. M.,
RA Glode A., Gorrell J.H., Gu Z., Galbart W.M., Glasser M.,
RA Glode A., Gorrell G.H., Re Z., Kennison J.A., Ketchum K.A.,
Alali M., Kalush F., Karpen G.H., Re Z., Kennison J.A., Ketchum K.A.,
Lau X., Mattei B., McIntoon T.C., Merim H., Inegwam C.,
RA Menson D.R., Nelson K.A., Howland T.S., Wei M., Wolkerson D.,
RA Melson D.R., Nelson K.A., Muxphy B., McDhecson D.,
RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
RA Spier E., Siden-Kiamos J., Simpson M., Strong R., Sung K.,
RA Shenert K., Remington K., Strong R., Wang X.,
RA Shenert K., Remington K., Strong R., Wang X.,
RA Shenert K., Remington K., Strong R., Wang X.,
RA Nalas R., Yackei B., Wollaw S., Pola S., Pola S., Pola S., Pola S.,
RA Shier B.C., Siden-Kiamos J., Simpson M., Strong R., Shen H.,
RA Shier B.C., Saderi J.S., Zhan M., Zhong W., Zhong Y., Wang S., Yao Q.A., Ye J.,
RA Sheng S., Rayeri J.S., Shon M., Zhong W., Zhong Y., Shon H., Shence S., Shen K., Bong S., Shon
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A Celniker S.E., Adams M.D., Amanatides P.G., Brandon R.C., Rogers Y.,

Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,

A carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.W.,

A Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.W.,

A Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.W.,

A Carlson J.W., Houck J., Hoshins R.A., Hostin D., Howland T.J.,

B Ferriers S., Frise E., Galle R.P., Margon N.S., George R.A.,

A Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,

A McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunco J.,

Phouanenavong S., Pittman G.S., Patel S., Pfeitfer B.,

Phouanenavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,

Stapleon M., Szrong R., Svirskas R., Tector C., Tyler D.,

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"Sequencing of Drosophila melanogaster genome.",

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                        Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
        Drosophila melanogaster (Fruit fly)
                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                           NCBI_TaxID=7227;
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86 LGGWLVDRAGRKLSLLLCSVPFVAGFAVITAAQDVMMLLGGRLLTGLACGVASLVAPVYI 145
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                                                S.E., Gibbs R.A., Rubin G.M., Venter C.J.; to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                            Length 471;
                                                                                                                                                                                                                                                                                                                                                                                                                       32.0%; Score 787; DB 5; Length 473
37.4%; Pred. No. 4.4e-45;
ive 91; Mismatches 167; Indels
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                               to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS50850; MFS; 1.
PROSITE; PS00217; SUGAR TRANSPORT 2; 1.
SEQUENCE 471 AA; 51323 MW; 33199A53BC0EF65B CRC64;
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Last sequence update)
Last annotation update)
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GO; GO: 10016020; C: membrane; IEA.

GO; GO: 1001531; F: sugar porter activity; IEA.

GO; GO: 1000531; F: sransporter activity; IEA.

GO; GO: 1000643; P: carbohydrate transport; IEA.

InterPro; IPR007114; MES.

InterPro; IPR003628; Sub transporter.

InterPro; IPR00363; Sugar transporter.

Pfam; PF00083; sugar tr: 1.

PRINTS; PR00171; SUGRTRNSPORT.
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                                                                                                                                             EMBL; AE003540; AAN11863.1;
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Compensers, Mesacota, Arthropoda; Insacra; Persygota;
Compensers, Mesacota, Arthropoda; Brachycera; Muscomorpha;
Compensers, Engobersygota, Diptera; Brachycera; Muscomorpha;
Compensers, Compensers,
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295
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                                                    --QGWEDPP 236
                                                                                                                         416 INWLMAFLVTKEFSSLMEVLRPYGAFWLASAFCIFSVLFTLFCVPETKGKTLEQITAHFE 475
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15 AGSWVGGIMPLAALAGGITGGPLIEYLGRRSTILATAVPFIVSSLLIACAVNVIMILCGR 74
                                                                                                                                                                         237 IGAEQSFHLALLRQPGIYKPFIIGVSLMAFQQLSGVNAVMFYAETIFEEA-KFKDSSLAS
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1 MTPEDPEETQPLLGPPGGSA......CVPETKGKTLEQITAHFEGR 477
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| cgn2_6/ptodata/2/pubpaa/USO0_PUBCOMB.pep:*
GenCore version 5.1.6
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result Query Arch Length DB ID Description

1 2457 100.0 477 12 US-10-168-651-1 Sequence 1, Appli 2 2450 99.7 477 12 US-09-886-954-1 Sequence 1, Appli 3 1491 60.7 326 15 US-10-169-395-9 Sequence 2093, Appli 6 948 38.6 50.7 14 US-10-169-395-9 Sequence 359, Appli 6 948 38.6 50.7 14 US-10-169-395-9 Sequence 110, Appli 772 28.6 50.7 16 US-10-169-395-9 Sequence 110, Appli 16 0.7 2 28.6 50.7 16 US-10-424-599-275264 Sequence 163544, 11 701-5 28.6 521 484 12 US-10-61-909-2 Sequence 163544, 11 701-5 28.6 523 12 US-10-425-114-59933 Sequence 59333, Appli 6 Sequence 5933, Appli 6 Sequence 163544, 11 701-5 28.6 523 12 US-10-425-114-59933 Sequence 36, Appli 16 US-10-425-114-59933 Sequence 36, Appli 16 US-10-191-114-5941 Sequence 36, Appli 16 US-10-191-114-5941 Sequence 36, Appli 16 US-10-191-114-5941 Sequence 11, Appli 15 US-10-094-059-4 Sequence 4, Appli 15 US-10-094-059-4 Sequence 4, Appli 15 US-10-094-059-4

Sequence 5, Appli	Sequence 46, Appl	Sequence 4, Appli	Sequence 4, Appli	Sequence 46, Appl	Sequence 170, App	Sequence 27, Appl	Sequence 14, Appl	Sequence 27, Appl	Seguence 27, Appl	Sequence 45, Appl	Sequence 166774,	Sequence 23371, A	Sequence 63791, A	Seguence 177463,	Sequence 63432, A	Sequence 29, Appl	Sequence 79, Appl	Sequence 74, Appl	Sequence 23536, A	Seguence 56366, A	Sequence 7, Appli	Sequence 63426, A	Sequence 42918, A	Sequence 28, Appl	Sequence 78, Appl	Seguence 73, Appl	Sequence 23552, A	Sequence 124519,	Sequence 20, Appl
4 US-10-170-528-5	4 US-10-162-012-46	4 US-10-062-960B-4	4 US-10-144-624-4	5 US-10-162-102-46	6 US-10-038-854-170	US-09-795-693-27	3 US-10-095-139-14	4 US-10-156-239-27	4 US-10-199-485-27	5 US-10-391-399-45	6 US-10-437-963-166774	5 US-10-369-493-23371	2 US-10-425-114-63791	6 US-10-437-963-177463	2 US-10-425-114-63432	3 US-10-024-623-29	4 US-10-154-419-79	4 US-10-146-733-74	5 US-10-369-493-23536	2 US-10-282-122A-56366	US-09-860-232A-7		2 US-10-282-122A-42918			4 US-10-146-733-73	5 US-10-369-493-23552	6 US-10-437-963-124519	US-09-795-693-20
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615	615	615	615	615	615	613.5	613.5	613.5	613.5	613.5	609.5	607	604.5	604.5	604.5	603	603	603	603	598.5	598	593.5	591.5	591.5	591.5	591.5	591.5	591.5	588.5
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### ALIGNMENTS

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US-10-168-651-1

Sequence 1. Application US/10168651

Sequence 1. Application US/10168651

Septimized 1. Application No. US20030171275A1

SEPTIMIZED TO USCOMATION:

APPLICANT: BAUGHY, Mariah R.

APPLICANT: BAUGHY, Mariah R.

APPLICANT: AU-YOUNG, Janice

APPLICANT: TAL JO, PAUGH ALIA M.

APPLICANT: TAL JO, PAUGH ALIA M.

APPLICANT: TALLAN, Danniel B.

APPLICANT: TALLAN, Danniel B.

APPLICANT: TALLAN, Danniel B.

APPLICANT: TANG, Y. Tom

APPLIC
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60.7%;
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NAME/KEY: MISC FEATURE
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Publication No. US20020038464A1

GENERAL INFORMATION:

APPLICANT: Charron, Maureen J.

TITLE OF INVENTION: NOVEL GLUCOSE TRANSPORTER/SENSOR PROTEIN AND USES THEREOF

TITLE OF INVENTION: NOVEL GLUCOSE TRANSPORTER/SENSOR PROTEIN AND USES THEREOF

CURRENT APPLICATION UNMERR: US/09/886,954

CURRENT FILING DATE: 2001-06-21

NUMBER OF SEQ ID NOS: 1

SOFTWARE: Patentin version 3.2
                                                                 ò
                                                                                                                                               61 APRLDDAAASWFGAVVTLGAAAGGVLGGWLVDRAGRKLSLLLCSVPFVAGFAVITAAQDV 120
                                                                                                                                                                   WMLLGGRLLTGLACGVASLVAPVYISEIAYPAVRGLLGSCVQLMVVVGILLAYLAGWVLE 180
                                                                                                                                                                                                                                121 WMLLGGRLLTGLACGVASLVAPVYISEIAYPAVRGLLGSCVQLMVVGILLAYLAGWVLE 180
                                                                                                                                                                                                                                                               181 WRWLAVLGCVPPSLMLLLMCFWPETPRFLLTQHRRQEAMAALRFLWGSEQGWEDPPIGAE 240
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                                                                                                            1 MIPEDPERTQFLLGFPGGSAPRGRRVFLAAFAAALGFLSFGFALGYSSPAIPSLQRAAPP
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                             100.0%; Score 2457; DB 14;
.larity 100.0%; Pred. No. 2.2e-208;
Conservative 0; Mismatches 0; 1
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Pred. No. 9.1e-208;
0; Mismatches 1;
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Best Local Similarity 99.8
Matches 476; Conservative
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                             Query Match
Best Local Similarity
Matches 477; Conserv
US-10-168-651-1
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US-09-886-954-1
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LOCATION: (249)
OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
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OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino
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                                                                                                                                                                                                                                                                                                                                                                                                                                  421 AFLVTKEFSSLMEVLRPYGAFWLASAFCIFSVLFTIFCVPETKGKTLEQITAHFEGR 477
WRWLAVLGCVPPSLMLLLMCFMPETPRFLLTQHRRQEAMAALRFLWGSEQGWEDPPIGAE
                                  241 QSFHLALLRQPGIYKPFIIGVSLMAFQQLSGVNAVMFYAETIFEEAKFKDSSLASVVVGV
                                                                                              QSFHLALLRQPGIYKPFIIGVSLMAFQQLSGVNAVMFYAETIFEEAKFKDSSLASVVVGV
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Publication No. US20040009491A1
GENERAL INFORMATION:
APPLICANT: Birse et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and
FILE REFERENCE: PA1311
CURRENT APPLICATION NUMBER: US/10/264,237
CURRENT FILING DATE: 2002-10-04
PRIOR FILING DATE: 2001-05-18
PRIOR FILING DATE: 2001-05-18
PRIOR FILING DATE: 2001-05-18
PRIOR FILING DATE: 2001-05-18
NUMBER OF SEQ ID NOS: 2876
SOFTHARE: Patentin Ver. 3.1
SEQ ID NO 2093
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Score 1491; DB 15; Length 326;

g ð pp  $\delta$ qq ŏ Db ð g

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APPLICANT: Yankovsky, N. K.
APPLICANT: Yankovsky, N. K.
APPLICANT: Kozlov, A. P.
APPLICANT: Lobashev, A. V.
APPLICANT: Krukovskaya, L. L.
TITLE OF INVENTION: In silico screening for phenotype-associated expressed sequences
FILE REFERENCE: 2760-103
CURRENT APPLICATION NUMBER: US/10/157,031
CURRENT FILING DATE: 2002-05-30
NUMBER OF SEQ ID NOS: 415
SOFTWARE: PATENTIN version 3.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   243 DVHWEFEQIQDNVRRQSSRVSWAEARAPHVCRPITVALLMRLLQQLTGITPILVYLQSIF 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               340 FKLTQGGPGNSSHVAISAPVS-----AQPVDASVG-LAWLAVGSMCLFIAGFAVGWGPI 392
181 WRWLAVLGCVPPSLMLLLMCFMPETPRFLLTQHRRQEAAPGLVRCGHGVQHECLRRLLQA 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                231 G--WEDPPIG---AEQSFHL--ALLROPGIYKPFIIGVSLMAFQQLSGVNAVMFYAETIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EEAKF----KDSSLASVVVGVIQVLFTAVAALIMDRAGRRLLLLVLSGVVMVFSTSAFGAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 507;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 80; Mismatches 166;
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42.7%; Pred. No. 5.5e-75;
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US-10-755-889-110
; Sequence 110, Application US/10755889
                                                                                                                                                                                                      ; Sequence 359, Application US/10157031
; Publication No. US20030108890A1
; GENERAL INFORMATION:
APPLICANT: Baranova, A. V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 42.7
Matches 216; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Homo sapiens
                                                  229 EQGW 232
                                                                              : ||
241 DPGW
                                                                                                                                                                 RESULT 5
US-10-157-031-359
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APPLICANT: KATO, Seishi
APPLICANT: KATO, Seishi
APPLICANT: KIMURA, Tomoko
TITLE OF INVENTION: THESE PROTEINS
FILE REFERENCE: 01997.015100.US
CURRENT APPLICATION NUMBER: US/10/169,395
CURRENT APPLICATION NUMBER: US/200-585
PRIOR FILING DATE: 2002-11-29
PRIOR APPLICATION NUMBER: JP 2000-588
PRIOR FILING DATE: 2000-01-06
PRIOR FILING DATE: 2000-01-06
PRIOR FILING DATE: 2000-01-01
PRIOR APPLICATION NUMBER: JP 2000-2299
PRIOR APPLICATION NUMBER: JP 2000-26862
PRIOR FILING DATE: 2000-01-01
PRIOR PRILING DATE: 2000-03-03
PRIOR FILING DATE: 2000-03-03
PRIOR FILING DATE: 2000-02-03
PRIOR PRILING DATE: 2000-02-03
PRIOR FILING DATE: 2000-12-28
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                                                                                                                                                                                                                                                                                                                                              403
                                                                                                                                                                                                                                                                                                                                                                                                                                                               241 HVKGVATGXCVLXNWLMXFLXTKEFSSLMEVLRPYGAFWLASAFCIFSVLFTLVCALKK 300
                                                                                                                                                                 283
                                                                                                                                                                                             EEAKEKDSSLASVVVGVIQVLFTAVAALIMDRAGRRILLIVISGVVNVFSTSAFGAVFKLT 343
                                                                                                                                                                                                                                                                                         QGGPGNSSHVAISAPVSAQPVDASVGLAWLAVGSMCLFIAGFAVGWGPIPWLLMSEIFPL 240
                                                                                                                                                                                                                                                                                                                                                                                                                                   HVKGVATGICVLTNWLMAFLVTKEFSSLMEVLRPYGAFWLASAFCIFSVLFTLFCVPBTK 463
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                                                                                                                       09
                                                                                                     1 MVVVGILLAYLAGWVLEWRWLAVLGCVPPSLMLLIMCFMPETPRFLLTQHRRQEAWAALR
                                                                                                                                                                 FLWGSEQGWEDPPIGAEQSFHLALLRQPGIYKPFIIGVSLMAFQQLSGVNAVMFYAETIF
                                                                                                                                                                                                                                                                                                                                              QCGPGNSSHVAISAPVSAQPVDASVGLAWLAVGSMCLFIAGFAVGWGPIPWLLMSEIFPL
                                                                            164 MVVVGILLAYLAGWVLEWRWLAVLGCVPPSLMLLLMCFMPETPRFLLTQHRRQEAMAALR
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                                  Gaps
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                                  Indels
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             Pred. No. 3.2e-123;
                                  1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 9, Application US/10169395
Publication No. US20040034192A1
GENERAL INFORMATION:
                96.38;
                                       Conservative
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Best Local Similarity
Matches 223; Conserv
                Best Local Similarity
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                                         289;
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CURRENT APPLICATION NUMBER: US/10/051,909
                       CURRENT FILING DATE: 2002-01-17
PRIOR APPLICATION NUMBER: 60/083,044
PRIOR FILING DATE: April 24, 1998
NUMBER OF SEQ ID NOS: 38
SOFTWARE: Microsoft Office 97
SEQ ID NO 38
LENGTH: 501
                                                                                                                                                                                                                                    Query Match 29.4
Best Local Similarity 35.6
Matches 173; Conservative
                                                                                                                                                         ; TYPE: PRT; ORGANISM: Oryza sativa
US-10-051-909-38
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ORGANISM: Glycine
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LENGTH: 484
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                             APPLICANT: Bristol-Wyers Squibb Company
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ASSOCIATED WITH THE NF-kB
TITLE OF INVENTION: PATHWAY
TITLE OF INVENTION: PATHWAY
FILE OF INVENTION: PATHWAY
FILE SEPERANCE: D0284 NP
CURRENT APPLICATION NUMBER: US/10/755,889
CURRENT FILING DATE: 2004-01-13
PRIOR APPLICATION NUMBER: US. 60/440,068
PRIOR FILING DATE: 2003-01-14
PRIOR FILING DATE: 2003-01-14
PRIOR FILING DATE: 2003-05-12
NUMBER OF SEQ ID NOS: 823
SOFTWARE: PATENTIN NOS: 823
SOFTWARE: PATENTIN VERSION 3:2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 284 BEAKF----KDSSLASVVVGVIQVLFTAVAALIMDRAGRRLLLVLSGVVMVFSTSAFGAY 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           231 G--WEDPPIG---AEQSFHL--ALLROPGIYKPFIIGVSLMAFQQLSGVNAVMFYAETIF 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     303 DSTAVLLPPKDD---AAIVGAVRLLSVLIAALTMDLAGRKVLLPVSAAIMFAANLTLGLY 359
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    393 PWLLMSEIFPLHVKGVATGICVLTNWLMAFLVTKEFSSLMEVLRPYGAFWLASAFCIFSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           360 IHF---GPRPLSPNSTAGLESBSWGDLAQPLAAPAGYLTLVPLLATMLFIMGYAVGWGPI
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                                                                                                                                                                                                                                                                                                                                                                                Length 507;
                                                                                                                                                                                                                                                                                                                                                                          38.6%; Score 948; DB 16; Length 507
42.7%; Pred. No. 5.5e-75;
live 80; Mismatches 166; Indels
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Publication No. US20020199217A1
GENERAL INFORMATION:
APPLICANT: Allen, Steve
APPLICANT: Helentjaris, Tim
APPLICANT: Hitz, Bill
APPLICANT: Tingey, Scott
TITLE OF INVENTION: Plant Sugar Transport Proteins
FILE REFERENCE: BB1163 US CIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LFTLFCVPETKGKTLEQITAHFE-GR 477
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                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 42.79
Matches 216; Conservative
                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Homo sapiens
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Sequence 275264, Application US/10424599
Publication No. US20040031072A1
SERNEAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Eavour Yillow
APPLICANT: Coo Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
                                                          8;
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                                                                                                                                                                                      63 RLDDAAAASWFGAVVTLGAAAGGVLGGWLVDRAGRKLSLLLCSVPFVAGFAVITAAQDVWM 122
                                                                                                                                                                                                                                                                                            182
                                                                                                                                                                                                                                                                                                                                                                                                          241 ------OSFHLALLRQPGIYKPFIIGVSLMAFQQLSGVNAVMFYAETIFEEAKF 288
                                                                                                                                                                                                                      KDSSLASVVVGVIQVLFTAVAALIMDRAGRRLLLVLSGVVMVFSTSAFGAYFKLTQGGPG 348
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                                                                                            17 GGSAPRGRRVFLAAFA-------AALGPLSFGFALGYSSPAIPSLQRAAPPAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     39 GGGGGMGSRLGSSAYSLRDSSVSAVLCTLIVALGPIQFGFTCGFSSPT----QDAIISDL
                                                                                                                                                                                                                                                                                                                270 EIKRSVQSSRRTITIRPADIKQKRYSVPLAVGIGLLVLQQLSGVNGILFYAASIFKAAGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       409 ATGICVLTNWLMAFLVTKEFSSLMEVLRPYGAFWLASAFCIFSVLFTLFCVPETKGKTLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             349 NSSHVAISAPVSAQPVDASVGLAWLAVGSMCLFIAGFAVGWGPIPWLLMSEIFPLHVKGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             52;
            Length 501;
                                                     Indels
29.4%; Score 723; DB 13; 35.6%; Pred. No. 4.2e-55; tive 89; Mismatches 172;
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; Sequence 63431, Application US/10425114
; Publication No. US20040034888A1
; Publication No. US2004003488BA1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Screen, Steven E
; APPLICANT: Application No. Screen, Steven E
; APPLICANT: Gao, Yongwei
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5313)B
; CURRENT APLICATION NUMBER: US/10/425,114
; NUMBER OF SEQ ID NOS: 73128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EIAYPAVRGLLGSCVQLMVVVGILLAYLAGWVLEWRWLAVLGCVPPSLMLLLMCFMPETP 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --OSFHLALLROPG 252
                                                                                    119 SGQMAEYIĞRKGSLMIAAIPNIIĞWLAISFAKDSSFLYMGRLLEĞFGVGVISYTVPVYIA 178
                                                                                                                                                                                                                       OSFHLALLROPG 252
                                                                                                                                                                                                                                                              239 RWLAKMNMMDDFETSLQVLRGFE----TDISAEVNDIKRAVASANKRTIRFQELNOKK 293
                                                                                                                                                                                                                                                                                                          253 IYKPFIIGVSLMAFQQLSGVNAVMFYAETIFEEAKFKDSSLASVVVGVIQVLFTAVAALI 312
                                                                                                                                                                                                                                                                                                                                                                                                 MDRAGRRLLLVLSGVVMVFSTSAFGAYFKLTQGGPGNSSHVAISAPVSAQPVDASVGLAW 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LAVGSMCLFIAGFAVGWGPIPWLLMSEIFPLHVKGVATGICVLTNWLMAFLVTKEFSSLM 432
FLCTLIVALGPIQFGFTGGFSSPTQDAIIRDLD----LTLSEFSVFGSLSNVGAMVGAIA 118
                                             87 GGWLVDRAGRKLSLLLCSVPFVAGFAVITAAQDVWMLLGGRLLTGLACGVASLVAPVYIS 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98
                                                                                                                                                         EIAYPAVRGLLGSCVQLMVVVGILLAYLAGWVLEWRWLAVLGCVPPSLMLLLMCFMPETP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EVLRPYGAFWLASAFCIFSVLFTLFCVPETKGKTLEQITAHF 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LSWSAGGTFVSYMVVSAFTLVFVILWVPETKGRTLEEIQWSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Clone ID: LIB4371-017-F11_FLI.pep
US-10-425-114-63431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 28.6%; Score 702; UB 12;
Best Local Similarity 35.9%; Pred. No. 3.2e-53;
Matches 166; Conservative 80; Mismatches 178;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RFLLTQHRRQEAMAALRFLWGSEQGWEDPPIGAE----
                                                                                                                                                                                                                     RFLLTQHRRQEAMAALRFLWGSEQGWEDPPIGAE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 63431
                                                                                                                                  147
                                                                                                                                                                            179
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Sequence 163544, Application US/10437963

Publication No. US20040123343A1

GENERAL INFORMATION:

APPLICANT: La Rosa, Thomas J.

APPLICANT: Cao, Yongwei

APPLICANT: Cao, Yongwei

APPLICANT: Cao, Yongwei

APPLICANT: Boukharov, Andrey A.

APPLICANT: Bribazuk, Brad

APPLICANT: Bribazuk, Brad

APPLICANT: Li, Ping

TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(53221)B

CURRENT APPLICATION NUMBER: US/10/437,963

CURRENT FILING DATE: 2003-05-14

NUMBER OF SEQ ID NOS: 204966

SEQ ID NO 163544
                                                                                                              7;
                                                                                                                                                                                         45 VLFCVLIVALGPIQFGFTCGYSSPTQGAIVRDL----NLSISBFSFFGSLSNVGAMVGAI 100
                                                                                                                                                                                                                                                                       PRWLAKMGMIDEFETSLOVLRGFD---TDISVEVHEIKRSVASTGKRAAIRFADLKRKRY 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             254 YKPFIIGVSLMAFQQLSGVNAVMFYAETIFEEAKFKDSSLASVVVGVIQVLFTAVAALIM 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DRAGRRILLLVLSGVVMVFSTSAFGAYFKLTQGGPGNSSHVAISAPVSAQPVDASVGLAWL 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         374 AVGSMCLFIAGFAVGWGPIPWLLMSEIFPLHVKGVATGICVLTNWLMAFLVTKEFSSLME 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DKSGRRLLLIISSSVMTVSLLIVSIAFYL-EGVVSEDSHL----FSILGIVSIVGLVAM 391
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                                                                                                                                                                                                                                            86 LGGWLVDRAGRKLSLILCSVPFVAGFAVITAAQDVWMLLGGRLLTGLACGVASLVAPVYI
                                                                                                                                                                                                                                                                                                                                                                                                                        ---GAEQSFHLALLRQPGI
                                                                                                                                                         26 VFLAAFAAALGPLSFGFALGYSSPAIPSLORAAPPAPRLDDAAASWFGAVVTLGAAAGGV
                                                                                                                                                                                                                                                                                                                                   SEIAYPAVRGLLGSCVQLMVVVGILLAYLAGWVLEWRWLAVLGCVPPSLMLLLMCFMPET
                                                                                                                34;
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                                                                    Length 484;
                                                                                                              89; Mismatches 174; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                434 VLRPYGAFWLASAFCIFSVLFTLFCVPETKGKTLEQITAHF 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -WSSGGTFTIYTVVAAFTIAFIAMWVPETKGRTLEEIQFSF 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Clone ID: PAT_MRT4530_62530C.1.pep
US-10-437-963-163544
    OTHER INFORMATION: Clone ID: PAT MRT3847 90584C.1.pep
                                                                                                                                                                                                                                                                                                                                                                                                                        PRFLLTQHRRQEAMAALRFLWGSEQGWEDPPI------
                                                                  29.1%; Score 716; DB 12; 35.6%; Pred. No. 1.7e-54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         =
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ORGANISM: Oryza sativa
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                                                                                       Best Local Similarity
Matches 164; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 9
US-10-437-963-163544
      ; OTHER INFORMATION
US-10-424-599-275264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       166;
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Best Local
                                                                       Query Match
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SEPHODER & BORW HA		QY 131 GLACGVASLVAPVYISEIAYPAVRGILGSCVOLMVVGILLAYLAGWYLENERLAVLGCV 190  DD 200 GFGVGIISYTVPVYIAEISPQNMRGALGSVNQLSVTFGIFLAYLLGWFIPWRLLAVIGAL 259  QY 191 PPSLMLLLMCFWPETPRFLLTQHRRQEAMAALRFLMGSEQGWEDPPFIGAE 240    :::	QY 241OSPHLALLRQPGIYKPFIIGVSLMAFQQLSGVNAVMFYAETIFEEAKFKDSSLASV 296  i 315 SSKRTTISFQELNQKKYRTPLLLGIGLLVLQNLSGINGVLFYASSIFKAAGVINSDLATC 374  QY 297 VVGVIQVLFTAVAALIMDRAGRRLLLVLSGVVNVFSTSAFGAFKLTQGGPGNSSHVAIS 356  i
Sequence 59933, Application US/10425114 Sequence 59933, Application US/204034888A1 GENERAL INFORMATION: APPLICANT: Liu, Jingdong APPLICANT: Liu, Jingdong APPLICANT: ADOL Xihua APPLICANT: Kovalic, David K. APPLICANT: Cao, Yongwei APPLICANT: Cao, Yongwei TITLE OF INVEXTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVEXTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVEXTION: Number: US/10/425,114 FILE REFERENCE: 38-21(53313)B CURRENT APPLICATION NUMBER: US/10/425,114 CURRENT FILING DATE: 2003-04-28 NUMBER OF SEQ ID NOS: 73128 SEQ ID NOS: 73128 TYPE: PRT ORGANISM: Zea mays TYPE: PRT ORGANISM: Zea mays FEATURE: CTHER INFORMATION: Clone ID: LIB3689-227-G11_FLI.pep	Query Match         28.6%; Score 701.5; DB 12; Length 509;           Best Local Similarity 34.2%; Pred. No. 3.4e-53;           Matches 173; Conservative 86; Mismatches 182; Indels 65; Gaps 8;           QY         10 QPLLGPPGGSAPRGRRVFLAAFAAALGPLSFGF 42           CA   Db         27 KPLINTGSWYRMPPAGGWMGSRQSSLMERLGSSAFSLRDVALSATLCTLIVALGPIQFGF 86	QY 43 ALGYSSPAIPSLQRAAPPAPRLDDAASWFGANVTLGAAAGGVLGGWLVDRAGRKLSLLL 102	OY 163 IMVVGILLAYLAGWVLEWRWLAVIGCVPPSLMLLIMCFMPETPRFLITQHRRQEAMAAL 222  203 LSVTIGILLAYLFGMFVPWRILAVLGILPCSILIPGLFFVPESPRWLAKMGKMEDFBYSL 262  C23 RFLWGSEQGWEDPPIGAEQSFHLALLRQPGIYKPFIIGVSLMAFQQ 268  223 RFLWGSEQGWEDPPIGAEQSFHLALLRQPGIYKPFIIGVSLMAFQQ 268  263 QVLRGFQTDITAEVNEIKRSLASSRRRTTIRFADIXQKRYSVPLVIGIGILVLQQ 317  269 LSGVNAVMFYAETIFEBAKFKDSSLASVVVGVIQVLFTAVAALIMDRAGRRLLLLVLGGVV 328  [

145 160 205 437

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---EWRWLAVLG--CVPPSLMLLLMCFMPETPRFLLTQHRRQEAMAALRFLWGSEQ-GWE 233
                                                                                                                      161 AEIAPKNIRGGLATINQLLIVIGGSVSFLLGSVINWRELALAGIVPCICLLVGLCFIPES 220
                                                                                                                                                                                                                                        ---LGAAAGGVLGGWLVDRAGRKLSLLLCSVPFVAGFAVITAAQ-----DVW----MLLGG 126
45 VLLSTLVAVCGSFTFGTCVGYSAPT---QAAIRADLNLSLAEFSMFGSLVTIGAMLGAI 100
                                                                                                                                                                                          221 PRWLAKVGREKEFQLALSRLRGKDADISDEAABILDYIETLQSLPKTKLLDLFQSKYVHS 280
                                                                                                                                                                                                                       257 FIIGVSLMAFQQLSGVNAVMFYAETIFEEAKFKDSSLASVVVGVIQVLFTAVAALIMDRA 316
                                                                                                                                                                                                                                                                                317 GRRLLLVLS--GVVMVFSTSAFGAYFKLTQGGPGNSSHVAISAPVSAQPVDASVGLAW-- 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 ALVAALGG---GFLFGYDTGVIGGFLALIDFLFRFGLLTSSGALAELVGYSTVLTGLVVS 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --SLORAAPPAPRLDDAAASWFGAVVT
                                                                                                                                                                                                                                                                                                                                                          146 SEIAYPAVRGLLGSCVQLMVVVGILLAYLAGWVLEWRWLAVLGCVPPSLMLLLMCFMPET
                                                                                                                                                            206 PRFLLTQHRRQEAMAALRFLWGSEQGWEDPP----IGAEQSF---HLALLRQPGIYKP
                                                                                                                                                                                                                                                                                                            ------DOSLLPEWVP
                                                                                                                                                                                                                                                                                                                                          373 -LAVGSMCLFIAGFAVGWGPIPWLLMSEIFPLHVKGVATGICVLTNWLMAFLVTKEFSSL
                                           86 LGGWLVDRAGRKLSLLLCSVPFVAGFAVITAAQDVWMLLGGRLLTGLACGVASLVAPVYI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 25.0%; Score 615; DB 12; Length 488; Best Local Similarity 35.0%; Pred. No. 1.4e-45; Matches 179; Conservative 74; Mismatches 168; Indels 9
                                                                                                                                                                                                                                                                                                                                                                                                     432 MEVLRPYGAFWLASAFCIFSVLFTLFCVPETKGKTLEQITA 472
                                                                                                                                                                                                                                                                                                                                                                                                                      341 GRRPLVMVSAAGTFLGCFVAAFAFFLK------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30 AFAAALGPLSFGFALGYSSPAIP-
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LENGTH: 488
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 14
US-09-794-822-11
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                       DB 15; Length 481;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IIILE OF INVENTION: Gene Sequences and Uses Thereof in Plants
      NWLMAFLVTKEFSSLMEVLRPYGAFWLASAFCIFSVLFTLFCVPETKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26.0%; Score 639; DB 15; Length 4 34.9%; Pred. No. 1e-47; ive 76; Mismatches 182; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE: 38-15(52796)B
CURRENT APPLICATION NUMBER: US/10/310,154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Madson, Linda L.
Malloy, Kathleen A.
McKiel, Christine L.
Miller, Philip W.
Padmayathi, Manchikanti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 60/337,358
PRIOR FILING DATE: 2001-12-04
                                                                         RESULT 13
US-10-310-154-725
US-10-310-154-725
Sequence 725, Application US/10310154
Publication No. US20030233670A1
GENERAL INFORMATION:
APPLICANT: Edgerton, Michael D
FERRAL OF THE FORMATION:
                                                                                                                                                                                                                                                                                                                                                          Galligan, Meghan M.
Hinchey, Brenda S.
Huang, Shihshieh
Johnson, G. Richard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Parnell, Laurence D. Start, William G.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Kretzmer, Keith A
Laccetti, Lucille B.
                                                                                                                                                                                                                                                                                   Boddupalli, Raghava
Deikman, Jill
Deng, Molian
                                                                                                                                                                 Chomet, Paul S.
Adams, Thomas H
Ruff, Thomas H
Agarwal, Ameeta K.
Ahrens, Jeffrey E.
Ball, James A.
Banu, G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Luethy, Michael M.
Lund, Adrian
                                                                                                                                                                                                                                                                                                                                 Dong, Jinzhuo
Duff, Stephen M.
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Zeng, Xiaoping
Zhang, Qiang
Zhao, Yajuan
Zhou, Li
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Tennesen, Dan
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Xin, Zhanguo
Xu, Nanfei
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SEQ ID NO 725
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; ORGANISM: Glycine max
US-10-310-154-725
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Best Local Simi
Matches 161;
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ALNSWGWRIPLGLQLVPALLLLIGLLFLPESPRWLVEKGKLEEAREVLAKLRGVEDVDQE 238
                                    -LLR---QPGIYKPFIIGVSLMAFQQLSGVNAVMFYA 279
                                                           239 IQEIXABLEATVSEEKAGKASWGELFRGRIRPKVRQRLLMGVMLQAFQQLTGINAIFYYS 298
                                                                                                     ETIFEEAKFKD----SSLASVVVGVIQVLFTAVAAL-IMDRAGRRLLLLVLSGVVMVFSTSA 335
                                                                                                                           299 PIIFKSVGVSDSVASLLVIIIVGVVNFVFTFVALIFLVDRFGRRPLLLLGAAGMAICFLI 358
                                                                                                                                                                                 394
                                                                                                                                                                                              359 LGA------SIGVALLILINKPKDPSSKAAGIVAIVFILLFIAFFALGWGPIPW 405
                                                                                                                                                                                                                                           LLMSEIFPLHVKGVATGICVLTNWLMAFLVTKEFSSLMEVLRPY--GAFWLA---SAFCI 449
                                                                                                                                                                                                                                                                           VILSELFPTKVRSKALALATAANWLANFII------GFLFPYITGAIGLALGGYVFLV 457
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---EWRWLAVLG---CVPPSLMLLLMCFMPETPRFLLTQHRRQEAMAALRFLWGSEQ-GWE 233
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ETIFEEAKFKD---SSLASVVVGVIQVLFTAVAAL-IMDRAGRRLLLVLSGVVMVFSTSA 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30 AFAAALGPLSFGFALGYSSPAIP-----SLQRAAPPAPRLDDAAASWFGAVVT 77
                                                                                                                                                                        FGAYFKLTQGGPGNSSHVAISAPVSAQPVDASVGLAWL-AVGSMCLFIAGFAVGWGPIPW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALVAALGG---GFLFGYDTGVIGGFLALIDFLFRFGLLTSSGALAELVGYSTVLTGLVVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Curtis, Rory A.J.
APPLICANT: Curtis, Rory A.J.
APPLICANT: Millennium Pharmaceuticals Inc.
TILLE OF INVENTION: 32468, A Human Sugar Transporter Family Member and
TITLE OF INVENTION: Uses Therefor
FILE REFERENCE: MIO1-040PIRM
CURRENT APPLICATION NUMBER: 05/10/094,059
CURRENT APPLICATION NUMBER: 60/275,053
PRIOR FILING DATE: 2001-03-12
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FASTENCE for Windows Version 4.0
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Pred. No. 1.4e-45;
4; Mismatches 168; Indels 90;
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FAGLLVLFILFVFFFVPETKGRTLEEIEELF
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Publication No. US20020127650A1
GENERAL INFORMATION:
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Best Local Similarity 35.0%
Matches 179; Conservative
                                    DPPIGAEQSFHLA-
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September 27, 2004, 19:24:47; Search time 34 Seconds (without alignments) 724.282 Million cell updates/sec
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1 MTPEDPEETQPLLGPPGGSA......CVPETKGKTLEQITAHFEGR 477
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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
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Perfect score:
Sequence:
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 200000000

1: /cgn2\_6/ptodata/2/jaa/5A COMB.pep:\*
2: /cgn2\_6/ptodata/2/jaa/5B\_COMB.pep:\*
3: /cgn2\_6/ptodata/2/jaa/6A\_COMB.pep:\*
4: /cgn2\_6/ptodata/2/jaa/6B\_COMB.pep:\*
5: /cgn2\_6/ptodata/2/jaa/PCTUS COMB.pep:\*
6: /cgn2\_6/ptodata/2/jaa/PCTUS COMB.pep:\* Issued\_Patents\_AA:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## STIMMARIES

SH	Description	-012-46 Sequence	-039A-11902 Sequence	9A-11933	-5 Sequence	9-5 Seguence	-5 Sequence	-10 Sequence	-549-10 Sequence	-417-10 Sequence	-686B-23 Sequence	-686B-18 Sequence	-392-6 Sequence	-549-6 Sequence	-417-6 Sequence	-686B-22 Sequence	2 Sequence	-686B-24 Sequence	-686B-16 Sequence	-692-13 Sequence	-972-13 Sequence 13,	-692-12 Sequence 12,	-972-12 Sequence 12,	-039A-11731 Sequence 117	-922-20 Sequence 20,	-844-3 Sequence	16126-3 Sequence 3,	•
SUMMAKIES	ΩI	US-10-162	US-09-489.	-09-489	-09 - 031	-299	-09-610	US-09-031	-09-299	US-09-610	$\sigma$	-09-679	-031	-09 - 29	US-09-610	US-09-679	19-60	-09-67	9-67	œ	US-09-339		US-09-339	US-09-489	US-09-291	US-08-355	PCT-US95-	
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Sequence 9, Appli Sequence 9549, App Sequence 4, Appli Sequence 4, Appli Sequence 19, Appli Sequence 10, Appli Sequence 10, Appli Sequence 26, Appli Sequence 24, Appli Sequence 28, Appli Sequence 28, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli	Sequence 11, Appl
US-09-894-927B-9 US-09-489-039A-9549 US-09-489-039-4 US-09-29-549-4 US-09-510-417-4 US-09-510-417-4 US-09-339-972-10 US-10-162-012-44 US-09-291-922-24 US-09-291-922-24 US-09-291-922-24 US-09-291-922-24 US-09-291-922-24 US-09-291-922-24 US-09-291-922-24 US-09-291-922-24 US-09-291-922-24 US-09-291-922-22	US-09-679-686B-21
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## ALIGNMENTS

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APPLICANT: CHILLS, ROLY A.J.
APPLICANT: SILOS-Sattiago, Immaculada
FILLE OF INVENTION NOVEL HUMAN ION CHANNEL AND TRANSPORTER FAMILY MEMBERS: US 101/162,012
CURRENT PRELICATION NUMBER: US 60/209,845
PRIOR PLILING DATE: 2000-06-05
PRIOR PLILING DATE: 2000-06-06
PRIOR PLILING DATE: 2000-06-05
PRIOR APPLICATION NUMBER: US 60/220,238
PRIOR PLILING DATE: 2000-06-05
PRIOR PLILING DATE: 2000-06-13
PRIOR PLILING DATE: 2000-06-13
PRIOR PLILING DATE: 2000-06-13
PRIOR PLILING DATE: 2000-06-13
PRIOR PRIOR APPLICATION NUMBER: US 60/229, 288
PRIOR PLILING DATE: 2000-06-13
PRIOR PRIOR APPLICATION NUMBER: US 60/290, 288
PRIOR APPLICATION NUMBER: US 60/290, 288
PRIOR PRIOR APPLICATION NUMBER: US 60/290, 288
PRIOR APPLICATION NUMBER: US 60/290, 288
                             ; Sequence 46, Application US/10162012; Patent No. 6682597; GENERAL INFORMATION:
US-10-162-012-46
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167 190 245

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301

421

393

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GENERAL INFORMATION:

APPLICANT: Gary Breton et. al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709,2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT APPLICATION NUMBER: US 60/117,747
PRIOR PILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----ASSGLSWLSVGMTMMCIAGYAMSAAPVVWILCSEIQPLKCRDFGITCSTTTNWVSN 449
                                                                                                                                                                             75 VVTLGAAAGGVLGGWLVDRAGRKLSLLLCSVPFVAGFAVITAAQDVWMLLGGRLLTGLAC 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                      288 ALFKINRNVRRAVFLGMLLQAMQQFTGMNIIMYYAPRIFKMAGFTTTEQOMIATLVVGLT 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         87 GGWLVDRAGRKISLLLCSVPFVAGFAVITAAQDVWMLLGGRLLIGLACGVASLVAPVYIS 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ||| :|| :|| || || || || || || || || || EIAPEKIRGSMISMYQLMITIGILGAYLSDTAFSYSGAWRWM.GVIIIPAVLLLIGUIFL 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   302 QVLFTAVAALIMDRAGRRLLLVLSGVVMVFSTSAFGAYFKLTQGGPGNSSHVAISAPVSA 361
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                                                                                             20 APRGRR-----VFLAAFAAALGPLSFGFALGYSSPAIPSLQRAAPPAPRLDDAAASWFGA
                                                                                                                           52 SPRIQRDTRRMNWFVSIAAAVAGLLFGLDIGVISGALPFITDHFTLSSQLQE----WVVS
                                                                                                                                                                                                            GVASLVAPVYISEIAYPAVRGLLGSCVQLMVVVGILLAYLAGWVLEW--RWLAVLG--CV
                                                                                                                                                                                                                                                                                       228 PAVILIILVVFLPNSPRWLAEKGRHIBABEVLRMLRDTSEKARDELNBIRESLKLKQGGW
                                                                                                                                                                                                                                                                                                                                                                                                                              246 ALLR-OPGIYKPFIIGVSLMARQQLSGVNAVMFYAETIFEEAKF---KDSSLASVVVGVI
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             Length 514;
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                                                      Indels
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          Query Match
24.6%; Score 605; DB 4; L
Best Local Similarity 33.3%; Pred. No. 9.1e-49;
Matches 156; Conservative 86; Mismatches 187;
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31.2%; Pred. No. 2.6e-46;
live 84; Mismatches 180;
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ORGANISM: Klebsiella pneumoniae
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Best Local Similarity 31.2%
Matches 149; Conservative
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
FILE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US/60/117,747
PRIOR PLILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 11902
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                                                                                                                                                                                                                                                             Length 488
                                                                                                                                                                                                                                                       Query Match
25.0%; Score 615; DB 4; Length 48
Best Local Similarity 35.0%; Pred. No. 9.5e-50;
Matches 179; Conservative 74; Mismatches 168; Indels
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          assigned)
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 11902, Application US/09489039A Patent No. 6610836
                                                                                                                                                                                          OTHER INFORMATION: consensus sequence
                                                                                                                                                                                                                                                                                                                                         30 AFAALGPLSFGFALGYSSPAIP--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-11902
                                                                                                                                TYPE: PRT
ORGANISM: Artificial Sequence
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                                                                                    SEQ ID NO 46
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                                                                                                                                                                        -----LALLRQPGIYKPFIIGVSLMAFQQLSGVNAVMFYAETIFEEAKFKDSSLASV 296
                                                                                                                                                                                              250 SQEKQVTVLELFRAPNYRQPIIISIMLQLSQQLSGINAVFYYSTGIFKDAGVQEPVYATI 309
                                                                                                                                                                                                                                                  297 VVGVIQVLFTAVAALIMDRAGRRLLLVLSGVVMVFSTSAFGAYFKLTQGGFGNSSHVAIS 356
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                                                                                                                                                                                                                                                                                                                                                                                                                             190 FIILPAIIQCAALPFCPESPRFLLINRKEEEKAKEILQRLWGTEDVAQDIQEMKDESMRM 249
                  133 ACGVASLVAPVYISEIAYPAVRGLLGSCVQLMVVVGILLAYLAGWVL----EWRWLAVLG 188
                                                                                              --CVPPSLMLLLMCFMPETPRFLLTQHRRQE-AMAALRFLWGSEQGWEDPPIGAEQSFH-
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APPLICANT: Weng, Xun
TITLE OF INVENTION: OLUTEX AND USES THEREOF
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESSE: Fish & Richardson P.C.
STREET: 225 Franklin Street
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SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
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26-APR-1999
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; Patent No. 6136547
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TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER: 09/05
FILING DATE: 26-FEB-1998
ATTORNEY/AGENT INFORMATION:
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amino acid
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INFORMATION FOR SEQ ID NO:
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MEDIUM TYPE: Diskett
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FILING DATE: 26-APF
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                                                                                                                                                        301 IQVLFTAVAALIMDRAGRRILLVLSGVVWVFSTSAFGAYFKLTQGGPGNSSHVAISAPVS 360
                                                                                                                                                                                          311 TNVLATFIAIGLVDRWGRKPTLILGFIVM----AAG-----MGVLGTMMHIGIHSSTA 359
                                                                                                                                                                                                                                361 AQPVDASVGLAWLAVGSMCLFIAGFAVGWGPIPWLLMSEIFPLHVKGVATGICVLTNWLM 420
--RFLWGSEQGWEDPPIGAEQSFH 244
                                                                                                                                                                                                                                                                       360 ------OYIÁVLMLLMFIVGFAMSAGPLIWVLCSEIQPLKGRDFGITCSTATNWIA 409
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                                                                                                                                                                                                                                                                                                             421 AFLVTKEFSSLMEVLRPYGAFWLASAFCIFSVLFTLFCVPETKGKTLEQITAH-FEGR 477
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                          Indels
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APPLICANT: Tartaglia, Louis A.
APPLICANT: Weng, Xun
TITLE OF INVENTION: NUCLEIC ACID MOLECULES
TITLE OF INVENTION: ENCODING GLUTEX AND USES THEREOF
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23.4%; Score 575.5; DB 2; 30.7%; Pred. No. 5.3e-46; ive 94; Mismatches 179;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: Windows95
SOFTWARE: FastSED for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/031,392
FILING DATE: 26-FEB-1998
ATTORNEY/AGENT INPORMATION:
RANNE: Maiklejohn, Ph.D., Anita L.
REGISTRATION NUMBER: 35,283
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Fish & Richardson P.C. STREET: 225 Franklin Street
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Sequence 5, Application US/09031392
Patent No. 5942398
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TELECOMMUNICATION INFORMATION:
    PETPRFLLTQHRRQEAMAAL-
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ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
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TELEFAX: 617/542-8906
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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APPLICANT: Weng, Xun
TITLE OF INVENTION: NUCLEIC ACID MOLECULES
TITLE OF INVENTION: ENCODING GLUTEX AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                               Query Match 23.4%; Score 575.5; DB 4;
Best Local Similarity 30.7%; Pred. No. 5.3e-46;
Matches 150; Conservative 94; Mismatches 179;
REFERENCE/DOCKET NUMBER: 07334/072002
                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-610-417-5
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
                 TELECOMMUNICATION INFORMATION
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
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18-09-031-392-10
Sequence 10, Application US/09031392
Patent No. 5942398
                                                                                                                                                                                                  LENGTH: 494 amino acids
                                                                                                     TELEX: 200154
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                          TYPE: amino acid
TOPOLOGY: linear
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COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                250 SQEKQVTVLELFRAPNYRQPIIISIMLQLSQQLSGINAVFYYSTGIFKDAGVQEPVYATI 309
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                                                                                                                                   ----QRAAPPAPRLDDAAASWFGAV
                                                                             Gaps
                                                                          65;
                    Length 494;
                                                                          Indels
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APPLICANT: Tartaglia, Louis A.
Weng, Xun
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING
GLUTEX AND USES THEREOF
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                 DB 3;
                                                                       94; Mismatches 179;
                 Score 575.5; DB 3
Pred. No. 5.3e-46;
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APPLICATION NUMBER: US/09/610,417
FILING DATE: 05-011-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/299,549
FILING DATE: <UMRTOWN
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 35,283
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ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
                                                                                                                             26 VFLAAFAAALGPLSFGFALGYSSPAIPSL--
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Patent No. 6346374
GENERAL INFORMATION:
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ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                 23.4%;
30.7%;
                                                                       Conservative
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461 ITRAFEGQ 468
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                                            Similarity
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                 Query Match
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                                         Best Loca
Matches
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66 WSLSVSIFAVGGMIGSFLVGXIGNRLGRKXAMLVNNVLAIAGGLLMGLAKXAXSFEMLIL 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SYSTEM: Windows95
FastSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                              07334/072002
                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Meiklejohn, Ph.D., Anita L. REGISTRATION NUMBER: 35,283
RESERENCE/DOCKET NUMBER: 07334/07;
TELECOMMUNICATION INFORMATION:
TELEPAX: 617/542-8906
                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/09/299,549
FILING DATE: 26-APR-1999
                                         Richardson P.C.
                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/031,392
FILING DATE: 26-FEB-1998
ATTORNEY/AGENT INFORMATION:
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
STREET: 225 Franklin Street
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ETKGKTLEQITAHF 474
                                                                                                                                                                                                   COMPUTER: IBM Compatible OPERATING SYSTEM: Window
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amino acid
                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                      Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ) MOLECULE TYPE: protein US-09-299-549-10
                                                                                                                                           ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                Boston
                                                                                                                            USA
                                                                                                                                                                                                                                                     SOFTWARE:
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                                                                                                                            COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   228 SEQGWEDPPIGAEQSFH-LALLRQPGIYKPFIIGVSLMAFQQLSGVNAVMFYABTIFEBA 286
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             87; Mismatches 160; Indels
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APPLICANT: Tarraglia, Louis A.
APPLICANT: Weng, Xun
TITLE OF INVENTION: UCCLEIC ACID MOLECULES ENCODING
TITLE OF INVENTION: GLUTEX AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    303 GVGQPVYATIGAGVVNTVFTVVSVFVVERAGRRTLHLL----
                   COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FASSEG for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/031,392
FILING DATE: 26-FEB-1998
ATTORNEY-AGENT INFORMATION:
NAME: Melklejohn, Ph.D., Anita L.
REGISTRATION NUMBER: 35,283
                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 07334/072001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 10, Application US/09299549
Patent No. 6136547
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ETKGRTFDEIAAAF 468
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amino acid
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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US-09-299-549-10
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Best Local S:
Matches 159
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347 PGNSSHVAISAPVSAQPVDASVGLAWLAVGSMCLFIAGFAVGWGPIPWLLMSEIFPLHVK 406
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----WYAIVVVLFICIYVAGFAWSWGPLGW 410
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                                                                                           342 LGGMAGCAVLMTIALALLDQVPWMSYVSIVAIFGFVAFFEVGPGPIPWFIVAELFSQGPR
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                                                                                                                                             407 GVATGICVLTNWLMAFLVTKEFSSLMEVLRPYGAFWLASAFCIFSVL-
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      303 GVGQPVYATIGAGVVNTVFTVVSVFVVERAGRRTIHLLL
                                                                                                                                                                                                                                                                                                                                                               Sequence 23, Application US/09679686B
Patent No. 6624343
GENERAL INFORMATION:
APPLICANT: Allen, Stephen M.
APPLICANT: Lightner, Jonathan E.
APPLICANT: Rafalski, J. Antoni.
APPLICANT: Rafalski, J. Antoni.
APPLICANT: Rafalski, J. Antoni.
APPLICANT: Robert Sequence Catherine J.
ITLE OF INVENTION: HEXOSE CARRIER PROTEINS
FILE REFRENCE: BB1160 US NA
CURRENT APPLICATION NUMBER: US/09/679,686B
CURRENT FILING DATE: 1998-04-09
PRIOR FILING DATE: 1998-04-09
PRIOR FILING DATE: 1999-04-09
PRIOR FILING DATE: 1999-04-07
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Microsoft Office 97
I DELING DATE: 1990-04-07
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ETKGRTFDEIAAAF 468
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US-09-679-686B-23
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Best Local S:
Matches 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---WRWLAVLGCVPPSLMLLLMCFMPETPRFLLTQHRRQEAMA--ALRFLWG---
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                                                                                                                                                                                                       ENCODING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 09/299,549
FILING DATE: curknown>
ATTORNEY/AGENT INFORMATION:
NAME: Weiklejohn, Ph.D., Anita L.
REGISTRATION NUMBER: 35,283
FRERENDE/DOCKET NUMBER: 07334/072002
TELECOMMUNICATION INFORMATION:
TELEFRAN
                                                                                                                                                                   AFFLLCALL Weng, Xun
TITLE OF INVENTION: NUCLEIC ACID MOLECULES F
GLUTEX AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM Compatible OPERATING SYSTEM: Windows95 SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/610,417
FILING DATE: 05-Jul-2000
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSER: Fish & Richardson P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
                                                                                                                                                            APPLICANT: Tartaglia, Louis A.
                                                                                           Sequence 10, Application US/09610417
Patent No. 6346374
GENERAL INFORMATION:
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TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 10:
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ETKGRTFDEIAAAF 468
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Matches 159; Conservative
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                                                                                                                                                                                                                                                                                                                           CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
                                                    RESULT 9
US-09-610-417-10
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TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             249 DVDISEEYADLUVASEES---KLVQHPWRNILQRKYRPQLIMAIMIPFFQQLTGINVIMF 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ENIAMLIVGRILLGVGVGFANQSVPVYLSEMAPARLRGMLNIGFQLMITIGILAAALINY 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               278 YAETIFEEAKFK-DSSLAS-VVVGVIQVLFTAVAALIMDRAGRRLLLVLSGVVMVFSTSA 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    306 YAPVLFETLGFKGDASLMSAVITGLVNVFATLVSVFTVDRLGRRKLFLOGGTOMLLSQLV 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            336 FGAYFKLTQGGPGNSSHVAISAPVSAQPVDASVGLAWLAVGSMCLFIAGFAVGWGPIPWL 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                36 VGTLIAVKFGTSG-----VGEMP----KGYAAAVVLFICLYVAGFAWSWGPLGWL 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       396 LMSEIFPLHVKGVATGICVLTNWLMAFLVTKEFSSLMEVLRPYGAFWLASAFCIFSVLFT 455
                    ----PRLDDAAASWFGAVVTLGAAAGGVLGGWLVDRAGRKLSLLLCSVPFVAGFAVITAA 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     71 ASQYCKYDNQLLQTFTSSLYLAALVSSFFAATVTRVVGRKWSMFTGGLTFLIGAALNGAA 130
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LLMSEIFPLHVKGVATGICVLTNWLMAFLVTKEFSSLMEVLRPYGAFWLASAFCIFSVLF 454
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 517;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22.1%; Score 542.5; DB 4;
29.9%; Pred. No. 7.4e-43;
tive 88; Mismatches 202;
                                                                                                                                                                                                                                                              APPLICANT: Allen, Stephen M.
APPLICANT: Lightner, Jonathan E.
APPLICANT: Lightner, Jonathan E.
APPLICANT: Rafalski, J. Antoni
APPLICANT: Thorpe, Catherine J.
TITLE OF INVENTION: HEXOSE CARRIER PROTEINS
FILE REFERENCE: BB1160 US NA
CURRENT APPLICATION NUMBER: US/09/679,686B
CURRENT FILING DATE: 1998-04-09
PRIOR PRLING DATE: 1998-04-09
PRIOR APPLICATION NUMBER: PCT/US99/07561
NUMBER OF SEQ ID NOS: 24
NUMBER OF SEQ ID NOS: 24
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                                                                                                                                                                                                       Sequence 18, Application US/09679686B Patent No. 6624343
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                                                                        455 TLFCVPETKGKTLEQI 470
                                                                                                  470 VFFLLPETKGIPIEEM 485
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                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                         US-09-679-686B-18
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51 IPSLQRAAPPAPRLDDAAASWFGAVVTLGA-----AAGGVLGGWLV----DRAGRKLSL 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               101 LLCSVPFVAG---FAVITAAQDVWMLLGGRLLTGLACGVASLVAPVYISEIAYPAVRGLL 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   210 -LTOHRROEAMAALRFL--WGSEOG----WEDPPIGAEOSFHLALLROPGI---YKPFII 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LLLVLSGVVMVFSTSAFGAYFKLTQGGPGNSSHVAISAPVSAQPVDASVGLAWLAVGSMC 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8 IGSEDGEPPQQRVTGTLVLAVFSAVLGSLQFGYNIGVINAPQKVIEQSYNETWLGRQGPE 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                      APPLICANT: Tartaglia, Louis A.
APPLICANT: Weng, Xun
TITLE OF INVENTION: NUCLEIC ACID MOLECULES
TITLE OF INVENTION: ENCODING GLUTEX AND USES THEREOF
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 21.8%; Score 536; DB 2; L
Best Local Similarity 30.5%; Pred. No. 3e-42;
Matches 159; Conservative 86; Mismatches 172;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: FASTSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13 LGPPGGSAPRGR---RVFLAAFAAALGPLSFGFA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Meiklejohn, Ph.D., Anita L.
REGISTRATION NUMBER: 35,283
REFERENCE/DOCKET NUMBER: 07334/072001
TELECOMMULICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JMBER: US/09/031,392
26-FEB-1998
                                                                                                                                                                                                                      Fish & Richardson P.C.
Sequence 6, Application US/09031392
Patent No. 5942398
GENERAL INFORMATION:
                                                                                                                                                                                                                                           STREET: 225 Franklin Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                             Windows95
                                                                                                                                                                                                                                                                                                                                                                                                                  IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 26-FEB-1998
ATTORNEY/AGENT INFORMATION:
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amino acid
                                                                                                                                                                                                                                                                                                                                      ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatibl
OPERATING SYSTEM: Windo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GPS---SIPP
                                                                                                                                                                                                                                                                                                                       USA
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173 GTLNQLAIVIGILIAQVLG--LESLLGTASLWPLLLGLTVLPALLQLVLLPFCPBSPRYL 230
                                                                                                                                                                                                               LLLVLSGVVMVFSTSAFGAYFKLTQGGPGNSSHVAISAPVSAQPVDASVGLAWLAVGSMC 379
                                                                                                                                                                                                                                                                                            380 LFIAGFAVGWGPIPWLLMSEIFPLHVKGVATGICVLTNWLMAFLVTKEFSSLMEVLRPYG 439
                                                                                                                                                                                                                                                                                                                                   390 GFVAFFEIGPGPIPWFIVAELFSQGPRPAAMAVAGFSNWTSNFIIGMGFQYVAEAMGPY- 448
                                                                                                                                                    291 AVVLQLSQQLSGINAVFYYSTSIFETAGVGQPAYATIGAGVVNTVFTLVSVLLVERAGRR
                                                                                 231 YIIQNLEGPARKSLKRLTGWADVSGVLAELKDEKRKLERERPLSLLQLLGSRTHRQPLÍÍ
                                                                                                                                                                                                                                           -LGYSSPA
                                             -LTQHRRQEAMAALRFL--WGSEQG----WEDPPIGAEQSFHLALLRQPGI---YKPFII
                                                                                                                               260 GVSLMAFQQLSGVNAVMFYAETIFEEAKFKDSSLASVVVGVIQVLFTAVAALIMDRAGRR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AFFLICTION: WENG, Xun
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING
GLUTEX AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                    ----VFLLFAVLLLGFFIFTFLRVPETRGRTFDOISAAF
                                                                                                                                                                                                                                                                                                                                                                              ----FTLFCVPETKGKTLEQITAHF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Meiklejohn, Ph.D., Anita L.
REGISTRATION NUMBER: 35,283
REFERENCE/DOCKET NUMBER: 07334/072002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13 LGPPGGSAPRGR---RVFLAAFAAALGPLSFGFA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Fish & Richardson P.C. STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/09/610,417
FILING DATE: 05-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 09/299,549
FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Tartaglia, Louis A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 6, Application US/09610417
Patent No. 6346374
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
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ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
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Best Local Similarity 30.5
Matches 159; Conservative
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  -GLAGMCGCAILMTVALLLLERVPAMSYVSIVAIF 389
                                      380 LFIAGFAVGWGPIPWLLMSEIFPLHVKGVATGICVLTNWLMAFLVTKEFSSLMEVLRPYG 439
                                                                  51 IPSLQRAAPPAPRLDDAAASWFGAVVTLGA-----AAGGVLGGWLV----DRAGRKLSL 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---WRWLAVLGCVPPSLMLLLMCFMPETPRFL 209
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 536; DB 3; Length 509;
Pred. No. 3e-42;
5; Mismatches 172; Indels 104; Gaps
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                                                                                                                                                                                                                                                                                                                        APPLICANT: Tartaglia, Louis A.
APPLICANT: Tartaglia, Louis A.
APPLICANT: Weng, Xun
TITLE OF INVENTION: UNCLEIC ACID MOLECULES ENCODING
TITLE OF INVENTION: GLUTEX AND USES THEREOF
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSEQ for Windows Version 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURENT APPLICATION DATA:
APPLICATION NUMBER: US/09/299,549
FILING DATE: 26-APR-1999
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/031,392
FILING DATE: 26-FEB-1998
ATTORNEY/AGENT INFORMATION:
NAME: Melklejohn, Ph.D., Anita L.
REGISTRATION NUMBER: 35,283
                                                                                                                                                                                                                                                                                                                                                                                                                                                       E: Fish & Richardson P.C. 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GSCVQLMVVVGILLAYLAGWVLE----
                                                                                                                                                                                                                                                                  Sequence 6, Application US/09299549
Patent No. 6136547
GENERAL INFORMATION:
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Conservative 86;
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TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER:
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amino acid
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein US-09-299-549-6
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STREET: 222
-mv. Boston
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Best Local Simi
Matches 159;
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US-09-299-549-6
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70 SWFGAVVTLGAAAGGVLGGWLVDRAGRKLSLLLCSVPFVAGFAVITAAQDVWMLLGGRLL 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              GPS---SIPP------GTLTTLWALSVAIFSVGGMISSFLIGIISQWLGRKRAM 112
                                                                                                                                       GSCVQLMVVVGILLAYLAGWVLE-----WRWLAVLGCVPPSLMLLLMCFMPETPRFL 209
                                                                                                                                                                                                                                                                                                             GVSLMAFQQLSGVNAVMFYAETIFEEAKFKDSSLASVVVGVIQVLFTAVAALIMDRAGRR 319
                                                 IPSLQRAAPPAPRLDDAAASWFGAVVTLGA-----AAGGVLGGWLV----DRAGRKLSL 100
                                                                                                               LLCSVPFVAG---FAVITAAQDVWMLLGGRLLJTGLACGVASLVAPVYISEIAYPAVRGLL 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KVFVTCFIGAFGGLIFGYDLGISGGVTSMEPFLEEFFPYVYKKMKSAHENEYCRFDSQLL
-LTQHRRQEAMAALRFL--WGSEQG----WEDPPIGAEQSFHLALLRQPGI---YKPFII
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RVFLAAFAAALGPLSFGFALGYSSPAI---PSLQRAAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Allen, Stephen M.
APPLICANT: Information:
APPLICANT: Lightner, Onathan E.
APPLICANT: Rafalski, J. Antoni
APPLICANT: Rafalski, J. Antoni
APPLICANT: Thorpe, Catherine J.
TITLE OF INVENTION: HEXOSE CARRIER PROTEINS
FILE REFERENCE: BB1160 US NA
CURRENT APPLICATION NUMBER: US/09/679,686B
CURRENT FILING DATE: 1998-04-09
PRIOR FILING DATE: 1998-04-09
PRIOR FILING DATE: 1999-04-07
NUMBER OF SEQ ID NOS: 24
SPECIARARE: Microsoft Office 97
SPG ID NO 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 22, Application US/09679686B Patent No. 6624343
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US-09-679-686B-22
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US-09-679-686B-22
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318 ASLLSAMVTGIIELLCTFVSVFTVDRFGRRILFLQGGIQMLVSQIAIGAMIGVKFGVAGT 377
                                                                                                                                                       422 AAQAINVSVNMFFTFLVAQLELTMLCHMK-FGLFFFFAFFVVIMTIFIYLMLDETKNVPI 480
                                                                                202 ISLGLACVPAVMIMIGALILPDTPNSLIERGYTEEAKEMLQSIRGTNEVDEEFQDLIDAS 261
                                                                                                                                EQS-----FHLALLRQPGIYKPFIIGVSLMA-FQQLSGVNAVMFYAETIFEEAKF--K 289
                                                                                                                                                                                                 290 DSSLASVVVGVIQVLFTAVAALIMDRAGRRLLLVLSGVVMVFSTSAFGAYF--KLTQGGP 347
                                                                                                                                                                                                                                                               GNSSHVAISAPVSAQPVDASVGLAWLAVGSMCLFIAGFAVGWGPIPWLLMSEIFPLHVKG 407
                                                                                                                                                                                                                                                                                                  421
                          142 LGFGVGFANQSVPVYLSEMAPPNLRGAFNNGFQVAIIFGIVVATIINYFTAQMKGNIGWR 201
                                                                                                                                                                                                                                                                                   WLAVLGCVPPSLMLLLMCFMPETPRFLLTQHRRQEAMAALRFLWGS---BQGWEDPPIGA
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TGLACGVASLVAPVYISEIAYPAVRGLLGSCVQLMVVVGILLAYLAGWV----
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Gapop 10.0 , Gapext 0.5
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geneseqp2002s:*
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Maximum Match 100%
Listing first 45 s
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Maximum DB seq length: 200000000
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Perfect score:
                                                                                                                                                                                                                                                Scoring table:
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                                                                                                                                                                                                               Sequence:
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                                                                                                          on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Description	Aae04888 Human tra	Abp58364 Human sol	CI.	9	m	Aab66934 Murine GL	Abb89717 Human pol	<u>о</u>	e	ω	1 GLUTX3	7	Aam93417 Human pol	Human	Abp58365 Human sol	Abp58363 Human sol		Abb63511 Drosophil			œ		Arab	9 Arabi	Arab
ΙD	AAE04888	ABP58364	AAB66932	AAB66939	AAB66933	AAB66934	ABB89717	AAE06579	ABU11283	AAB66938	AAB66941	AAB66937	AAM93417	ADA84077	ABP58365	ABP58363	AAM93364	ABB63511	ABB65350	ABB63758	ABB62408	ABB57922	AAG13749	AAG13748	AAG13750
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Length	477	477	477	478	478	477	326	262	248	503	507	507	507	507	507	507	445	489	539	433	465	497	447	463	437
% Query Match	100.0	100.0	9.66	90.5	88.0	87.5	60.7	46.2	46.0	39.5	8	Θ.	38.6	æ	æ	38.6	9	2	32.1	31.1	σ	28.7	7.	27.3	27.2
Score	2457	4	2448	2224.5	2162.5	2150	1491	1135	1131	969.5	953	948	948	948	948	948	894	788.5	788	764.5	727	705	670	670	669.5
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Abbs8057 Drosophil Aag20977 Arabidops					Aag38871 Arabidops			Abp98504 PFAM cons	Aae35306 Human sug	Add22918 Human sug	Abg73334 Consensus	Abp52164 E. coli a	Add37502 E. coli a	Pro		Abul4994 Protein e	Add37501 E. coli g	Abu31194 Protein e
ABB58057 AAG20977	AAG20976	AAG20978	AAG38870	AAG38869	AAG38871	ABB65373	ABB57923	ABP98504	AAE35306	ADD22918	ABG73334	ABP52164	ADD37502	ABU28442	ABP52163	ABU14994	ADD37501	ABU31194
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4 4 4 4 4 4	463	437	448	464	438	491	491	488	488	488	487	472	472	465	464	464	464	453
27.1	26.9	26.9	26.6	26.6	26.5	26.3	26.3	25.0	25.0	25.0	25.0	24.5	24.5	24.4	24.1	24.1	24.1	23.8
666.5	662	661.5	652.5	652.5	652	647	647	615	615	615	613.5	603	603	598.5	591.5	591.5	591.5	585.5
26	28	53	30	31	32	33	34	i M	36	37	38	39	40	41	42	4.3	44	45

## ALIGNMENTS

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AAE04888 standard; protein; 477

RESULT 1 AAE04888

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Human; transporter and ion channel-1; TRICH-1; vaccine; cystic fibrosis; gene therapy; amyotrophic lateral sclerosis; amnesia; muscular dystrophy; hypertension; angina; neurological disorder; asthma; bipolar disorder; profementia; depression; Alzheimer; disease; epilepsy; mood, arrhythmia; pick's disease; ischaemic cerebrovascular disease; AIDS; anxiety; stroke; Huntington's disease; mental disorder; Schizophrenia; polymyositis; demyelinating disease; mental disorder; Schizophrenia; polymyositis; drabetes mellitus; immunological disorder; psoriasis; theumatorid arthritis; Sjogren's syndrome; systemic lupus erythematosus; sickle cell anaemia; Wilson's disease; scleroderma; pulmonary artery stenosis; infertility; Cushing's disease; malabsorption syndrome; hypercholesterolaemia; cancer.
                                                                       Human transporter and ion channel-1 (TRICH-1) protein.
                                                                                                                                                                                                                                                                                                                                                         29. .474
/note= "Sugar transporter domain"
259. .279
                                                                                                                                                                                                                                                                                                                                                                                                                     293. .313
/label= Transmembrane_domain
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/label= Transmembrane_domain
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14-JAN-2000; 2000US-0176083P.
21-JAN-2000; 2000US-0177332P.
28-JAN-2000; 2000US-0178572P.
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                                            (first entry)
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                                                                                                                                                                                                                                                                                                                 Homo sapiens
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                                           10-SEP-2001
               AAE04888;
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The present sequence is transporter and ion channel-1 (TRICH-1) protein.

TRICH is used as vaccine. TRICH is useful for treating a disease or condition associated with decreased expression of functional TRICH, such as transport disorder including amyotrophic lateral sclerosis, cystic fibrosis, Becker's muscular dystrophy, angina and hypertension, neurological disorders including Alzheimer's disease, amnesia, bipolar disorder, disorder, arrow prince, creptoral neoplasms, plck's disease, imental disorder, muscle carnot, andien, depression, epilepsy, ischaemic cerebrovascular disease, and disorder including disease, mental disorder, muscle barkinson's disease, demyelinating disease, mental disorder, muscle cardiomyopathy, myocarditis, polymyositis, arrhythmias and sasonal affective disorder, muscle dermatomyositis, arrhythmias and asthma and immunological disorders including AIDS, adult respiratory distress syndrome (ARDS), allergies, anaemia, diabetes mellitus, rheumatoid arthritis, scleroderms, syndrome, systemic lupus erythematosus and other diseases including sickle cell anaemia, Wilson's disease, Castracts, infertility, pullmonary contents sendiorisis, Grave's disease, Cushing's disease, Addison's disease, psoriasis and viral, bacterial, fungal, helmthic and protozoal currects infections. TRICH DNA is useful in gene therapy and in diagnostic
                                                                                                  Lu DAM, Yang J, Reddy R;
H, Nguyen DB, Yao MG, Gandhi AR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241 QSFHLALLRQPGIYKPFIIGVSLMAFQQLSGVNAVMFYAETIFEEAKFKDSSLASVVVGV 300
                                                                                                                                                                                                                                  proteins useful for treating and
                                                                                                                                                                                                                                           preventing transport, neurological, muscle and immunological disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MTPEDPEETQPILGPPGGSAPRGRRVFLAAFAAALGPLSFGFALGYSSPAIPSLQRAAPP
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                                                                                                                                                                                                                      Novel human transporter and ion channel
                                                                                                                                                                                                                                                                                 Claim 1; Page 112-113; 160pp; English.
                                                                                                  J,
                                                                                                V, Au-Young
Azimzai Y,
02-FEB-2000; 2000US-0179758P.
                                                       (INCY-) INCYTE GENOMICS INC.
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Lal P, Hillman JL,
Tang YT, Khan FA;
                                                                                                                                                                       WPI; 2001-418042/44.
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Identifying candidate p53 pathway modulating agent as therapeutic target for disorders of defective p53 function e.g. cancer, by assaying purified solute carrier family 2 (SLC2A) polypeptide or nucleic acid with a test
                                                                                                                                       Human, solute carrier type 2A; SLC2A; glucose transporter; p53; cancer; cytostatic; gene therapy.
          Funke RP;
421 AFLVTKBFSSLMBVLRPYGAFWLASAFCIFSVLFTLFCVPBTKGKTLBQITAHFEGR
                                                                                                                       Human solute carrier type 2A polypeptide 12735153 and 7657681
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N-PSDB; ABZ24792, ABZ24793, ABZ24794.
                                                                                                                                                                                        location/Qualifiers
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                                                                ABP58364 standard; protein; 477 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-JUN-2001; 2001US-0296076P.
10-OCT-2001; 2001US-0328605P.
15-FEB-2002; 2002US-0357253P.
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/note= "t-
68
                                                                                                     (first entry)
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127. .149
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                                                                                                                                                                      Homo sapiens.
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                                                                                  ABP58364;
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IQVLFTAVAALIMDRAGRRLLLVLSGVVMVFSTSAFGAYFKLTQGGPGNSSHVAISAPVS 360 

301

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AQPVDASVGLAWLAVGSMCLFIAGFAVGNGPIPWLLMSEIFPLHVKGVATGICVLTNWLM 420

Σ Uldry

Ibberson M,

'n,

Thorens

(UYLA-) UNIV LAUSANNE

14-JUL-1999; 99US-0143907P. 27-AUG-1999; 99US-0151140P. 23-FEB-2000; 2000US-0184285P. 13-JUL-2000; 2000US-00616132.

14-JUL-2000; 2000WO-IB001042

WO200104145-A2 Homo sapiens

18-JAN-2001

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The present sequence is that of human solute carrier type 2A (SLC2A) polypeptides 12735153 and 7657681. In the present invention, genetic screens were designed to identify modifiers of the p53 pathway in prosophila in which p53 and solverspressed. Human orthologues

Crosophila in which p53 assolverspressed. Human orthologues

(polynucleotides and polypeptides) of one such modifier were then identified, including the present polypeptides. SLC2As are glucose transporter proteins with sugar transporter domains. They are attractive drug targets for treatment of pathologies associated with a defective p53 signalling pathway, such as cancer. The invention provides in vitro and in vivo methods of assessing SLC2A function. Modulation of an SLC2A or its binding partners is useful for understanding the association of the p53 pathway and its members in normal and disease conditions and for developing diagnostic and therapeutic modalities of p53-related pathologies. SLC2A-modulating agents that act by inhibiting or enhancing SLC2A expression, directly or indirectly, e.g. by affecting an SLC2A function such as transport or binding activity, can be identified using methodies, antisense oligonucleotides and phosphothioate morpholino
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hypoglycaemia; glucose metabolism disorder; neurodegenerative disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                           Length 477;
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Pred. No. 5.1e-227;
; Mismatches 0;
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Best Local Similarity 100.
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                                                                                                                                       SAQPVDASVGLAWLAVGSMCLFIAGFAVGWGPIPWLLMSEIFPLHVKGVATGICVLTNWL 419
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                                                                                301 IIQVLFTAVAALIMDRAGRRLILALSGVIMVFSMSAFGTYFKLTQSGPSNSSHVGILVPI
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No. 9.9e-199;
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                                                                                                                                                                                    GLUTX, gene therapy; vaccine, hexose transport modulator; human; rat; hexose transport disorder; ischaemia; diabetes; hyperglycaemia; murine; hypoglycaemia; glucose metabolism disorder; neurodegenerative disease.
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Pred. No. 1.1e-204;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 11; Page 74-75; 124pp; English.
                                       Ä.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Uldry M;
                                       standard; protein; 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27-AUG-1999; 99US-0151140P.
23-FEB-2000; 2000US-0184285P.
13-JUL-2000; 2000US-00616132.
                                                                                                                                                                                                                                                                                                                                                                                                                   14-JUL-2000; 2000WO-IB001042
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                                                                                                                (first entry)
                                                                                                                                                   GLUTX1 consensus sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    prevention, diagnosis ischemia and diabetes.
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                                                                                                                                                                                                                                                                                                                                        WO200104145-A2.
                                                                                                                                                                                                                                                               Homo sapiens
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                                                                                                              17-APR-2001
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                                                                                                                                                                                                                                                                                                    Rattus sp.
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                                                    SAQPVDASVGLAWLAVGSMCLFIAGFAVGWGPIPWLLMSEIFPLHVKGVATGICVLTNWL 419
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic acids encoding GLUTX glucose transporter proteins, useful in the prevention, diagnosis and treatment of hexose transport disorders, e.g. ischemia and diabetes.
                                                                                                                                                                                                                                                             477
                                                                                                                                                                                                                                                                                    478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to GLUTX proteins (AAF55865-AAF55871 and AAB66932-AAB66941). The GLUTX proteins are related to the facultative glucose carriers GLUT1-GLUT5 and have hexose binding and/or transport
          ALRLGDTAASWFGAVVTLGAAAGGVLGGWLLDRAGRKLSLLLCTVPFVTGFAVITAARDV
                                                                                                Murine; GLUTX; gene therapy; vaccine; hexose transport modulator; hexose transport disorder; ischaemia; diabetes; hyperglycaemia; hypoglycaemia; glucose metabolism disorder; neurodegenerative disease.
                                                                                                                               -OSFHLALLROPGIYKPFIIGVSLMAFQQLSGVNAVMFYAETIFEEAKFKDSSLASVVVG
APRLDDAAASWFGAVVTLGAAAGGVLGGWLVDRAGRKLSLLLCSVPFVAGFAVITAAQDV
                                                                                     WRWL, AVLGCVPPSLMLLLLMCFMPETPRFLLTQHRRQEAMAALRFLWGSEQGWEDPPIGAE
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B; AAF55867.
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23-FEB-2000;
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function. The GLUTX proteins may be used in the diagnosis, prevention and treatment of hexose transport disorders such as ischaemia, diabetes, hyperglycaemia, hypoglycaemia, a glucose metabolism disorder and/or a neurodegenerative disease. The present sequence is murine GLUTXI
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                                                                                                                      2;
                                                                                            Length 477;
                                                                                                                     Indels
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                                                                                           87.5%; Score 2150; DB 4;
85.6%; Pred. No. 1.6e-197;
live 33; Mismatches 34;
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                                                                                         Query Match
Best Local Similarity 85.6
Matches 409; Conservative
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06-JAN-2000; 2000JP-0000588. 11-JAN-2000; 2000JP-00002299. 03-FEB-2000; 2000JP-00026862. 03-MAR-2000; 2000JP-00058367.

28-DEC-2000; 2000WO-JP009359.

WO200149728-A2. Homo sapiens.

12-JUL-2001.

2000JP-00000585

06-JAN-2000;

(SAGA ) SAGAMI CHEM RES CENT.

Kato S,

WPI; 2001-418355/44. N-PSDB; AAD12574.

(PROT-) PROTEGENE INC

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Human; hydrophobic domain; gene therapy; nutritional supplement; cell proliferation; immunomodulatory; autoimmune disorder; antimicrobial; multiple solerosis; rheumatoid arthritis; insulin-dependent diabetes; haematopoiesis; tissue growth activity; Parkinson's disease; cytostatic; Huntington's disease; Altheimer's disease; chemotactic; chemokinetic; haemostatic; thrombolytic; tumour growth inhibitor; anabolic; contraceptive; antiinfertility; antiinflammatory.
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                                                             prevention of neural, immune system, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal and proliferative
                                               Novel 1405 isolated polypeptides, useful for diagnosis, treatment
                                                                                                            Claim 11; SEQ ID NO 2093; 2081pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                            Length 326;
                                                                                                                                                                                                                                                                                                                                                                                                                    10; Indels
                                                                                                                                                                                                                                                                                                                                                                                       Score 1491; DB 5;
Pred. No. 1.9e-134;
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                                                                                                                                                                                                                                                                                                                                                                                       60.7%;
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           2002-122018/16
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                      N-PSDB; ABL90126
                                                                                                                                                                                                                                                                                                                                                                Sequence 326 AA;
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                                                                                     disorders
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The present sequence is human protein with hydrophobic domain, HP10784.

The polynucleotide and polypeptide of the invention may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate polypeptide expression. The polynucleotides may be used to produce the polypeptide, by inserting the nucleic acids into a host cell and culturing the cell to express the protein. The polynucleotides and cits complementary sequences may also be used as Sasays and also used in gene therapy. The polypeptides may also be used as antigens in the production of antibodies and in assays to identify modulators of polypeptide expression and activity. The polypeptides and nucleic acids may be used as nutritional supplements, to modulate conclude a could be used as antigens in the production activity, to modulate immune stimulation or suppression (e.g. for the treatment of microbial infections and autoimmune disorders such as multiple sclerosis, rheumatoid arthritis and tissue growth activity (e.g. for the treatment of Parkinson's disease, thuntingron's disease and Albaheme's disease, to modulate activity and chemokinetic activity, to modulate haemostatic and chemokinetic activity, to modulate haemostatic and chemokinetic activity, to modulate haemostatic and thrombolytic activity, to modulate haemostatic and chemokinetic activity, to modulate haemostatic and chemokinetic activity, to modulate haemostatic and chemokinetic activity, to modulate haemostatic and inflammation and to inhibit tumour growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human proteins with hydrophobic domains and the nucleic acids encoding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MIPEDPEETQPLLGPPGGSAPRGRRVFLAAFAAALGPLSFGFALGYSSPAIPSLQRAAPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MTPEDPEETQPLLGPPGGSAPRGRRVFLAAFAAALGPLSFGFALGYSSPAIPSLQRAAPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 APRLDDAAASWFGAVVTLGAAAGGVLGGWLVDRAGRKLSLLLCSVPFVAGFAVITAAQDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 APRLDDAAASWEGAVVTLGAAAGGVLGGWLVDRAGRKLSLLLCSVPFVAGFAVITAAQDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 WMLLGGRLLTGLACGVASLVAPVYISEIAYPAVRGLLGSCVQLMVVVGILLAYLAGWVLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WRWLAVLGCVPPSLMLLLMCFMPETPRFLLTQHRRQBAM-------AALRFLWGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          them, useful for preventing diagnosing and treating e.g. cancer, Alzheimer's and inflammation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         46.2%; Score 1135; DB 4; I
01 4%; Pred. No. 2.2e-100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 75; 563pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               223; Conservative
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                                                                                                                                                                                                                                                      2000US-00616132
                  AAB66938 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 43.6%
Matches 212; Conservative
                                                           entry
                                                                                                                                                                                                                                                                                               Ibberson M,
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                                                          (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 503 AA;
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27-AUG-1999;
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                                                          17-APR-2001
                                                                                                                                                                                 18-JAN-2001
                                                                                                                                                                                                                                                                                               В,
                                                                              Rat GLUTX3
                                                                                                                                           Rattus sp.
                                      AAB66938;
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                                                                                                                                                                                                                                                                                                                                                                                                         protein with cancer suppressing function. The invention also comprises a method for preparing the polypeptide by recombination, and an application of the polypeptide in treating diseases such as cancer, etc. Also disclosed in an antagonist of the polypeptide and its medical action. The present sequence represents a cancer suppressing protein of the invention
                                                                                                                                                                                                                                                                                                                                                                                                  cDNA and protein sequences of a novel human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  164 MVVVGILLAYLAGWVLEWRWLAVLGCVPPSLMLLLMCFMPETPRFLLTQHRRQEAMAALR 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EBAKFKDSSLASVVVGVIQVLFTAVAALIMDRAGRRLLLVLSGVVMVFSTSAFGAYFKLT 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QGGPGNSSHVAISAPVSAQPVDASVGLAWLAVGSMCLFIAGFAVGWGP-IPWLLMSEIFP 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FLWGSEQGWEDPPIGAEQSFHLALLRQPGIYKPFIIGVSLMAFQQLSGVNAVMFYAETIF 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FLWGSEQGWEDPPIGAEQSFHLALLRQPGIXKPFIIGVSLMAFQQLSGVNAVMFYAETIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MVVVGILLAYLAGWVLEWRWLAVLGCVPPSLMLLIMCFWPETPRFLLTQHRRQEAMAALR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EEAKFKDSSLASVVVGVIQVLFTAVAALIMDRAGRRLLLVLSGVVMVFSTSAFGAYFKLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                               New human protein with cancer cell growth suppressing function and
                                                                                                                                                                                                                                                                                                                                                          polynucleotide encoding it, for treating diseases, such as, cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 248;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                               cancer suppressing protein PP7425.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 1131; DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. 5e-100;
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 23 (disclosure); 39pp; Chinese.
                                                                                                                                                   Human; cancer suppressing protein; cancer
                                                                    ABU11283 standard; protein; 248 AA
                                                                                                                                                                                                                                                                         (SHAN-) SHANGHAI INST ONCOLOGY
                                                                                                                                                                                                                                                                                                                                                                                                 This invention relates to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          46.0%;
93.0%;
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                                                                                                                                                                                                                                 31-OCT-2000; 2000CN-00127102
                                                                                                             entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                           (first
                                                                                                                               human
                                                                                                                                                                                                                                                                                                                  2002-609437/66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LHLQ 239
232
                  244
                                                                                                                                                                                                                                                                                                                  WPI; 2002-609437,
N-PSDB; ABX34029.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 248 AA;
            :
DPGW
                                                                                                                               cDNA encoding
EOGW
                                                                                                                                                                                                                                                      31-OCT-2000;
                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                              29-MAY-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             227;
                                                                                                            10-FEB-2003
                                                                                                                                                                                           CN1351081-A
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                                                                                        ABU11283;
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229
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                  241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RLDKIQASWFGSVFTLGAAAGGLSAMLLNDLLGRKLSIMFSAVPSAIGYALMAGARGLWM 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LLGGRLLTGLACGVASLVAPVYISEIAYPAVRGLLGSCVQLMVVVGILLAYLAGWVLEWR 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LLIGRMITGFAGGLTAACIPVYVSEIAPPGVRGALGATPOLMAVFGSLSLYALGLLLPWR 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acids encoding GLUTX glucose transporter proteins, useful in the prevention, diagnosis and treatment of hexose transport disorders, e.g. ischemia and diabetes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62
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Rat; GLUTX; gene therapy; vaccine; hexose transport modulator;
hexose transport disorder; ischaemia; diabetes; hyperglycaemia;
hypoglycaemia; glucose metabolism disorder; neurodegenerative disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----KARAGALQNRRVFLATFAAVLGNFSFGYALVYTSPVIPALKRSSDPAL
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43.6%; Pred. No. 4.2e-84;
live 80; Mismatches 175;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 11; Page 82-83; 124pp; English
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           312 DAAIVGAVRLLSVLIAAVIMDLAGRKVLLYVSASIMFVANLTLGLYVQLVPRTLIPNSTV 371
                                              411
                                                                    431
                                                                                       412 ICVLTNWLMAFLVTKEFSSLMEVLRPYGAFWLASAFCIFSVLFTLFCVPETKGKTLEQIT 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to GLUTX proteins (AAF55865-AAF55871 and AAB66932-AAB66941). The GLUTX proteins are related to the facultative glucose carriers GLUTI-GLUTS and have hexose binding and/or transport function. The GLUTX proteins may be used in the diagnosis, prevention and treatment of hexose transport disorders such as ischaemia, diabetes, hyperglycaemia, hypoglycaemia, a glucose metabolism disorder and/or a neurodegenerative disease. The present sequence is a consensus sequence
                                                                                                       in the
                                                                                                                                                                                                                                                                                                          GLUTX; gene therapy; vaccine; hexose transport modulator; human; rat; hexose transport disorder; ischaemia; diabetes; hyperglycaemia; hypoglycaemia; glucose metabolism disorder; neurodegenerative disease.
ASVVVGVIQVLFTAVAALIMDRAGRRLLLVLSGVVMVFSTSAFGAYFKLTQG--GPGNSS
                                                          HVAISAPVSAQPVDASVGLAWLAVGSMCLFIAGFAVGWGPIPWLLMSEIFPLHVKGVATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        e transporter proteins, useful i of hexose transport disorders,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 507;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  38.8%; Score 953; DB 4; Length 50 42.9%; Pred. No. 1.6e-82; ive 78; Mismatches 167; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JTX glucose
treatment o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 11; Page 83-84; 124pp; English.
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                                                                                                                                                                                                                    protein; 507
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99US-0151140P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                       14-JUL-2000; 2000WO-IB001042
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                                                                                                                                                                                                                                                                                     GLUTX3 consensus sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ischemia and diabetes.
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                                                                                                                                                                                                                    standard;
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27-AUG-1999;
23-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic acids
                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13-JUL-2000;
                                                                                                                                                                                                                                                               17-APR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    prevention,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Thorens B,
                                                                                                                                                                                                                                                                                                                                                                      SD.
                                                                   372
                                                                                                                                                                                                                                        AAB66941;
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294
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11;

Gaps

44;

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Similarity

Best Local Sımı Matches 217;

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122
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                         62
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                 IPSLORAAPPAPRLDDAAASWFGAVVTLGAAAGGVLGGWLVDRAGRKLSLLLCSVPFVAG
  ---RVFLAAFAALGPLSFGFALGYSSPA
                                                                                                                      SLYALGILLPWRWLAVAGXAPVLIMILLISFWPNSPRFILESRGRDEBALRALAWLRGTDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human, GLUTX; gene therapy; vaccine; hexose transport modulator;
hexose transport disorder; ischaemia; diabetes; hyperglycaemia;
hypoglycaemia; glucose metabolism disorder; neurodegenerative disease.
                                                                63 IPALERSLDPDLHLTKSQASWFGSVFTLGAAAGGLSAMILNDLLGRKLSIMFSAVPSAAG
                                                                                                                                                                                                                                                                                                                                                                                     FAVITAAQDVWMLLGGRLLTGLACGVASLVAPVYISEIAYPAVRGLLGSCVQLMVVVGIL
                                                                                                                                                       LAYLAGWVLEWRWLAVLGCVPPSLMLLLMCFMPETPRFLLTQHRRQEAMAALRFLWGSEQ
                                                                                                                                                                                                            G--WEDPPIG---AEQSFHL--ALLRQPGIYKPFIIGVSLMAFQQLSGVNAVMFYAETIF
                                                                                                                                                                                                                                   DVHWEFGQIQDNVRRQSSRVSWAEARAPHVCRPITVALLMRLLQQLTGITPILVYLQSIF
                                                                                                                                                                                                                                                             284 EEAKF----KDSSLASVVVGVIQVLFTAVAALIMDRAGRRLLLVLSGVVVVVFSTSAFGAY
                                                                                                                                                                                                                                                                           FKLTQGGPGNSSHVAISAPVS-----AQPVDASVG-LAWLAVGSMCLFIAGFAVGWGPI
                                                                                                                                                                                                                                                                                                                                 IHF---GPRRLSPNSTAGLESESWGDLAQPLAAPAGYLTLVPLLATMLFIMGYAVGWGPI
                                                                                                                                                                                                                                                                                                                                                                  PWLLMSEIFPLHVKGVATGICVLTNWLMAFLVTKEFSSLMEVLRPYGAFWLASAFCIFSV
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  ---PPGGSAPRGR-
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27-AQC-1999; 99US-0151140P.
23-FEB-2000; 2000US-0184285P.
13-JUL-2000; 2000US-00616132.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              standard;
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 OPLIG-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human GLUTX3
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07-JUL-2000; 2000EP-00114089
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                                     The present invention relates to GLUTX proteins (AAF55865-AAF55871 and AAB66322-AAB66941). The GLUTX proteins are related to the facultative glucose carriers GLUT1-GLUT5 and have hexose binding and/or transport function. The GLUTX proteins may be used in the diagnosis, prevention and treatment of hexose transport discorders such as isohaemia, diabetes, hyperglycaemia, hypoglycaemia, a glucose metabolism discorder and/or a neurodegenerative disease. The present sequence is human GLUTX3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LAYLAGWVLEWRWLAVLGCVPPSLMLLLMCFMPETPRFLLTQHRRQEAMAALRFLWGSEQ 230
                                                                                                                                                                                                                                                                                                                                                 EEAKF----KDSSLASVVVGVIQVLFTAVAALIMDRAGRRILLLVLSGVVMVFSTSAFGAY 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                         PWILMSEIFPLHVKGVATGICVLTNWLMAFLVTKEFSSLMEVLRPYGAFWLASAFCIFSV 452
                                                                                                                                                                                                                                    IPALERSLDPDLHLTKSQASWFGSVFTLGAAAGGLSAMILNDLLGRKLSIMFSAVPSAAG 122
                                                                                                                                                                                                                                                                            YAVMAGAHGLWMLLLGRTLTGFAGGLTAACIPVYVSEIAPPGVRGALGATPQLMAVFGSL 182
                                                                                                                                                                            20
                                                                                                                                                                                              EPLICAEGPDYDTFPEKPPPSPGDRARVGTLONKRVFLATFAAVLGNFSFGYALVYTSPV 62
                                                                                                                                                                                                                                                                                                            SLYALGLILPWRWLAVAGXAPVLIMILLLSFMPNSPRFLLSRGRDEEALRALAWLGTDV
                                                                                                                                                                                                                                                                                                                                                                                        IHF---GPRPLSPNSTAGLESESWGDLAQPLAAPAGYLTLVPLLATMLFIMGYAVGWGPI
                                                                                                                                                                            --RVFLAAFAALGPLSFGFALGYSSPA
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                                                                                                                                                                                                                                                          FAVITAAQDVWMLLGGRLLTGLACGVASLVAPVYISEIAYPAVRGLLGSCVQLMVVVGIL
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                                                                                                                                                        Gaps
                                                                                                                                                         44;
                                                                                                                                     Length 507;
                                                                                                                                     38.6%; Score 948; DB 4; Length 50' 42.9%; Pred. No. 4.9e-82; ive 78; Mismatches 167; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; full length cDNA; cDNA synthesis; oligo-capping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 502
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                                                                                                                                                                            PPGGSAPRGR--
                   11; Page 81-82; 124pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein;
                                                                                                                                               Local Similarity 42.9
les 217; Conservative
  diabetes
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  and
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                   Claim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             clones. 830 cDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5' and 3'-ends of the cDNA molecules have been determined. Primers for synthesising the full length cDNA molecules have been determined. Primers for synthesising the full length cDNA are useful length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence is a polypeptide encoded by a full length not form part of the invention. Note: The sequence data for this patent did format directly from EPO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IPALERSLDPDLHLTKSQASWFGSVFTLGAAAGGLSAMILNDLLGRKLSIMFSAVPSAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SLYALGLLLPWRWLAVAGEAPVLIMILLSFMPNSPRFLLSRGRDEEALRALAWLRGTDV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --RVFLAAFAALGPLSFGFALGYSSPA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                            invention relates to primers for synthesising full length cDNA
                                                                                                                                                  Hayashi K, Ishii S, Kawai Y;
K, Kojima S, Otsuki T, Koga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            44;
                                                                                                                                                                                                                                                                                                             synthesizing full length cDNA clones
                                                                                                                                                                                                                                                                                                                                                                                           Claim 8; SEQ ID NO 3034; 1380pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 507;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           38.6%; Score 948; DB 4; Length 50 42.7%; Pred. No. 4.9e-82; Live 80; Mismatches 166; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              477
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                                                                                                                                                       Isogai T,
T, Nagai
99JP-00194486.
                        2000JP-00118774.
                                                      2000JP-00183765
                                                                                                                                                                                   Wakamatsu A, Sugiyama T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                               O Primers useful for a
genetic manipulation
                                                                                                       (HELI-) HELIX RES INST
                                                                                                                                                                                                                                   WPI; 2001-524255/58.
N-PSDB; AAK94338.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 216; Conserv
                                                                                                                                                          Nishikawa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 507 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPLIG-
  08-JUL-1999;
                                11-JAN-2000;
                                                      02-MAY-2000;
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Human solute
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a novel method for determining if a nucleic acid is a marker for a predetermined phenotype/cell type of interest from a biological species. The method comprises performing a global comparison of a group of expressed sequence tags (ESTS) known to be expressed in the comparison of a group of interest with all ESTS expressed in the comparison of in order to identify ESTS that are preferentially expressed in the phenotype/cell type of interest of the invention is useful for determining whether a nucleic acid is a marker for a predetermined phenotype or cell type of interest from a biological species, preferably arabidopsis or human. The cell type of interest is an abnormal cell such as a tumour cell, and the predetermined phenotype is a stress-induced phenotype such as hyperosmotic stress or high salt conditions. A method of the invention is also useful for detecrining the progression of colon cancer in a human, for detecting a tumour cell, and for regulating or preventing the growth of a tumour cell. An antibody of the invention is useful for detecting a tumour cell, and for regulating or tumour-associated markers. A polypeptide of the invention is useful as an immunogen for vaccinating an animal. The present sequence represents a concert in a number of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EPLIGAEGPDYDTFPEKPPPSPGDRARVGTLQNKRVFLATFAAVLGNFSFGYALVYTSPV 62
                                                                                                                                           human; marker; expressed sequence tag; EST; arabidopsis; tumour; stress-induced phenotype; hyperosmotic stress; colon cancer; immunogen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Determining if a nucleic acid is a marker for a phenotype/cell type of interest, by global comparison of expressed sequence tags known to be expressed in the phenotype/cell type with all ESTs expressed in normal
                                                                                                                                                                                                                                                                                                                                                                                                                                     Lobashev AV, Krukovskaya LL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RVFLAAFAALGPLSFGFALGYSSPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 507;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 948; DB 6; Length 50
Pred. No. 4.9e-82;
); Mismatches 166; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                    Kozlov AP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 29; Page 458-460; 516pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10 QPLLG------PPGGSAPRGR-
                ADA84077 standard; protein; 507 AA.
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                                                                                                                                                                                                                                                                                                                                     30-MAY-2001; 2001US-0293999P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 42.7%;
Matches 216; Conservative 80
                                                                                                                                                                                                                                                                                                                                                                                                                                    Yankovsky NK,
                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                  (BIOM-) BIOMEDICAL CENT
                                                                                                               protein.
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                                                                                                                                                                                                                                      WO2002103028-A2.
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                                                                                                             Human SLC2A6
                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                Baranova AV,
                                                                              20-NOV-2003
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                                                ADA84077;
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ADA8407
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51 IPSLQRAAPPAPRLDDAAASWFGAVVTLGAAAGGVLGGWLVDRAGRKLSLLLCSVPFVAG 110

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170
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63 IPALERSLDPDLHLTKSQASWFGSVFTLGAAAAGGLSAMILNDLLGRKLSIMFSAVBSAAG 122
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                                                                                                                                                                                                                                  392
                                                                                                                                                                                                                                                                                  452
                                                                                                                                                                                                                                                                                               Human; solute carrier type 2A; SLC2A; glucose transporter; p53; cancer; cytostatic; gene therapy.
                                                                                  171 LAYLAGWVLEWRWLAVLGCVPPSLMLLLMCFMPETPRFLLTQHRRQEAMAALRFLWGSEQ
                                                                                                   SLYALGLILPWRWLAVAGEAPVLIMILLSFWPNSPRFILSRGRDEEALRALAWLRGTDV
                                                                                                                                                                                  BEAKF----KDSSLASVVVGVIQVLFTAVAALIMDRAGRRLLLVLSGVVMVFSTSAFGAY
                                   111 FAVITAAQDVWMLLGGRLLTGLACGVASLVAPVYISBIAYPAVRGLLGSCVQLMVVVGIL
                                                  G--WEDPPIG---AEQSFHL--ALLRQPGIYKPFIIGVSLMAFQQLSGVNAVMFYAETIF
                                                                                                                                                  243 DVHWEFEQIQDNVRRQSSRVSWAEARAPHYCRPITVALLMRLLQQLTGITPILVYLQSIF
                                                                                                                                                                                                360 IHF---GPRPLSPNSTAGLESESWGDLAQPLAAPAGYLTLVPLLATMLFIMGYAVGWGPI
                                                                                                                                                                                                                               340 FKLTQGGPGNSSHVAISAPVS-----AQPVDASVG-LAWLAVGSMCLFIAGFAVGWGPI
                                                                                                                                                                                                                                                                                PWLLMSEIFPLHVKGVATGICVLTNWLMAFLVTKEFSSLMEVLRPYGAFWLASAFCIFSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "sugar transporter domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          carrier type 2A polypeptide 8923733.
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458. .480
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191. .213
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279. .301
/note= "transmembrane
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
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391. .413
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The present sequence is that of human solute carrier type 2A (SLC2A) polypeptide 89237334. In the present invention, genetic screens were designed to identify modifiers of the p53 pathway in Drosophila in which p53 was overexpressed. Human orthologues (polynucleotides and polypeptides) of one such modifier were then identified, including the present polypeptide SLC2As are glucose transporter proteins with sugar transporter domains. They are attractive drug targets for the treatment of pathologies associated with a defective p53 signalling pathway, such as cancer. The invention provides in vitro and in vivo methods of assessing SLC2A function. Modulation of an SLC2A or its binding partners is useful for understanding the association of the p53 pathway and its members in normal and disease conditions and for developing diagnostic and therapeutic modaltries of p53-related pathologies. SLC2A-modulating agents that act by inhibiting or enhancing SLC2A expression, directly or indirectly, e.g. by affecting an SLC2A function such as transport or indirectly, e.g. by affecting an SLC2A function such as transport or binding activity, can be identified using methods provided. Modulators include small molecules, nucleic acids, antibodies, antisense oligonucleotides and phosphothioate morpholino oligomers (claimed)
                                                                                                                                                                                                                                                                                                                                                                                                         Identifying candidate p53 pathway modulating agent as therapeutic target for disorders of defective p53 function e.g. cancer, by assaying purified solute carrier family 2 (SLC2A) polypeptide or nucleic acid with a test
                                                                                                                                                                                                                                                                                                                    Funke RP;
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/note= "transmembrane domain"
                                                                                                                                                                                                                                                                                                                 Belvin M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 13; Page 48-50; 58pp; English.
                                                                                                                                                                               05-JUN-2001; 2001US-0296076P.
10-OCT-2001; 2001US-0328605P.
15-FEB-2002; 2002US-0357253P.
                                                                                                                                    03-JUN-2002; 2002WO-US017419
                                                                                                                                                                                                                                                                                                                 Plowman GD,
                                                                                                                                                                                                                                                                       (EXEL-) EXELIXIS INC
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                                             WO200298467-A1
                                                                                                                                                                                                                                                                                                                    Friedman L,
                                                                                          12-DEC-2002
#XWX#X###X#X#X#X#X#X######X
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171 LAYLAGWVLEWRWLAVLGCVPPSLMLLLMCFMPETPRFLLTQHRRQEAMAALRFLWGSEQ 230
                                                                                                                                                                                                                                                                                                                   SLYALGLLLPWRWLAVAGEAPVLIMILLLSFMPNSPRFLLSRGRDEEALRALAWLRGTDV 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   303 DSTAVLLPPKDD---AAIVGAVRLLSVLIAALTWDLAGRKVLLFVSAAIMFAANLTLGLY 359
                                                                                                                                                IPSLORAAPPAPRLDDAAASWFGAVVTLGAAAGGVLGGWLVDRAGRKLSLLLCSVPFVAG 110
                                                                                                                                                                   FAVITAAQDVWMLLGGRLLTGLACGVASLVAPVYISEIAYPAVRGLLGSCVQLMVVVGIL 170
                                                                                                                                                                                                                                                            182
                                                                                                                                                                                                                                                                                                                                                                      G--WEDDPIG---AEQSFHL--ALLRQPGIYKPFIIGVSLMAFQQLSGVNAVMFYAETIF 283
                                                                                                                                                                                                                                                                                                                                                                                                                                              284 EEAKF----KDSSLASVVVGVIQVLFTAVAALIMDRAGRRLLLVLSGVVMVFSTSAFGAY 339
                                                                                              -PPGGSAPRGR-----RVFLAAFAALGPLSFGFALGYSSPA 50
                                                                                                                                                                                                                                                                                                                                                                                               123 YALMAGAHGLWMLLLGRTLTGFAGGLTAACIPVYVSEIAPPGVRGALGATPQLMAVFGSL
                                       44;
 Length 507;
38.6%; Score 948; DB 6; Length 507
42.7%; Pred. No. 4.9e-82;
ive 80; Mismatches 166; Indels
                                       Conservative
                    Similarity
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Query Match
Best Local Simi
Matches 216;
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392
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                           360 IHF---GPRPLSPNSTAGLESESWGDLAQPLAAPAGYLTLVPLLATMLFIMGYAVGWGPI
340 FKLTQGGPGNSSHVAISAPVS-----AQPVDASVG-LAWLAVGSMCLFIAGFAVGWGPI
                                                                                   PWILMSEIFPLHVKGVATGICVLTNWLMAFLVTKEFSSLMEVLRPYGAFWLASAFCIFSV
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time

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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protein search, using sw model OM protein September 27, 2004, 19:22:56; Search time 45 Seconds (without alignments) 1019.630 Million cell updates/sec Run on:

Title: Perfect score:

US-09-886-954A-1 2457 1 MTPEDPEETQPLLGPPGGSA.......CVPETKGKTLEQITAHFEGR 477 BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table: Seguence:

283366 segs, 96191526 residues Searched:

283366 of hits satisfying chosen parameters: Total number

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

summaries Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 su

PIR 78:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

		ď				
Result No.	Score	Query Match	Length	DB	ID	Description
	734	. 2	! !	5	E96782	hypothetical prote
7	722	29.		7	T14545	probable sugar tra
ю	607	24	461	~	D70073	metabolite transpo
4	607	24	471	~	AB0868	L-arabinose isomer
Ŋ	606.5		4	7	S47089	н
9	603	24		7	B26430	L-arabinose isomer
7	603	24.		7	B91091	L-arabinose isomer
80	603	24	472	7	E85936	L-arabinose isomer
σ	591.5	24		7	F65079	galactose-proton s
10	587.5	23	4	7	Oi	galactose-proton s
11	587.5	23		7	F85951	galactose-proton s
12	584.5	23		~	T52132	probable sugar tra
13	584.5		575	7	T43400	myo-inositol trans
14	583.5	23		7	AC0877	galactose-proton s
15	582			N	G84864	probable membrane
16	574.5	23.		~	S38981	glucose transport
17	570.5	23.	2 496	7	A31986	glucose transporte
18	569.5	23.		~	A41751	glucose transport
19	567	23.			D86426	hypothetical prote
20	560.5	22.			E70070	metabolite transpo
21	556.5	22.	9 560		ഹ	sugar transporter-
22	S	22.(			F69587	L-arabinose transp
23	551	22.4			G85059	probable sugar tra
24	48.	22.	52	7	S25015	monosaccharide tra
25	546.5	22	52	N	T01853	probable hexose tr
26	546	22.:		~	A26430	xylose transport p
27	546	22.:	49	۲	$\overline{}$	xylose-proton symp
28	546	22 . :	49	7	8609	xylose-proton symp
29	542.5	22	1 522	N	A31556	glucose transport

hexose transport p	glucose transport	gracose transport monosaccharid tran	muscle-fat glucose	probable sugar-pro	glucose transporte	probable sugar tra	monosaccharide tra	probable sugar tra	glucose transport	glucose transport	probable sugar tra	hexose transport p	glucose transport	glucose transport	hearded transmort n
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22.1 534		21.9	21.8	21.8	21.8	21.8	21.8	21.7	21.7	21.6	21.6	21.6	21.6	21.6	
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## ALIGNMENTS

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Arabidopsis thaliana E96782 hypothe

C; Species: Arabidopsis thalian a mouse-car cress)
C; Species: Arabidopsis thalian a mouse-car cress)
C; Date: 02-Mar-2001
C; Date: 02-Mar-2001
B; Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, C; Accession. B96782
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.B.; Creasy, T.H.; Dewar, K. ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A; Authors: Hunter, J.L.; Vi, Lin, X.; Liu, Z.A.; Luros, J.S.; Khaykin, B.; Kim, C.C.; J. in, Y.; Lin, Y.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A; Authors: Salzberg, S.L.; Schwartz, J.S.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A; Reference number: A86141; MUID:21016719; PMID:11130712
A; Status: prellminary
A; Molecule type: DNA
A; Residues: 1-487 <STO>
A; Cross-references: GB:AB005173; NID:g10092276; PIDN:AAG12689.1; GSPDB:GN00141

A; Gene: F22H5.6

A; Map position: 1 C; Superfamily: glucose transport protein

9 Gaps 34; 29.9%; Score 734; DB 2; Length 487; 37.5%; Pred. No. 8.9e-47; Indels ative 77; Mismatches 177; Indels Query Match 29.9% Best Local Similarity 37.5% Matches 173; Conservative

103 85 48 VLACVLIVALGPIQPGFTCGYSSPT----QAAITKDLGLTVSEYSVFGSLSNVGAMVGAI 26 VFLAAFAAALGPLSFGFALGYSSPAIPSLORAAPPAPRLDDAAASWFGAVVTLGAAAGGV g ò

163 145 86 LGGWLVDRAGRKLSLLLCSVPFVAGFAVITAAQDVWMLLGGRLLTGLACGVASLVAPVXI à 셤

205 146 SEIAYPAVRGLLGSCVOLMVVVGILLAYLAGWVLEWRWLAVLGCVPPSLMLLLMCFMPET à d

-----SFHLALLRQPGI 253 224 PRWLAKMGMIDEFETSLQVLRGFE---TDITVEVNEIKRSVASSTKRNTVRFVDLKRRY 280 PRFLLTQHRRQEAMAALRFLWGSEQGWEDPPIGAEQ-206 à Dp YKPFIIGVSLMAFQQLSGVNAVMFYAETIFEEAKFKDSSLASVVVGVIQVLFTAVAALIM 313 254 ð g

314 DRAGRRILLIVLSGVVMVFSTSAFGAYFKLTQGGPGNSSHVAISAPVSAQPVDASVGLAWL 373 ð

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L-arabinose isomerase [imported] - Salmonella enterica subsp. enterica serovar Typhi (st
C;Species: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C;Accession: AB0868
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
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C; Species: Beta vulgaris (beet)
C; Date: 20-Sep.1999 #sequence_revision 20-Sep-1999 #text_change 21-Jul-2000
R; Chiou, T.J. Bush, D.R.
Plant Physiol. 110, 511-520, 1996
A; Title: Wolcoular cloning, immunochemical localization to the vacuole, and expr A; Reference number: 218131; MUID:96351183; PMID:8742332
A; Reference number: 218131; MUID:96351183; PMID:8742332
A; Residues: preliminary; translated from GB/EWBL/DDBJ
A; Cross-references: EMBL:043629; NID:g1209755; PIDN:AAB53155.1; PID:g1209756
C; Superimental source: tonoplast protein
C; Keywords: transmembrane protein
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         :| | | : | ---FVSPDS----DMYSWLSIL 386
                                                                  AVGSMCLFIAGFAVGWGPIPWLLMSEIFPLHVKGVATGICVLTNWLMAFLVTKEFSSLME 433
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            82
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C;Species: Bacillus subtilis
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 20-Jun-2000
                                                                                              :| : |::| | | | | :|:| |:| ::| ::|: 387 SVVGVVAMVVPFSLGMGPIPWLIMSEILPVNIKGLAGSIATLANWFFSWLITMT-ANLLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ASGQISEYIGRKGSLMIAAIPNIIGWLAISFAXDSSFLYMGRMLEGFGVGIISYTVPVYI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       281 RYWLPLMIGNGLLILQQLSGINGVLFYSSTIFKEAGVTSSNAATFGLGAVQVIATVVTTW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VLACVLIVALGPIQFGFTAGYSSPT----QSAITNELGLSVAEYSWFGSLSNVGAMVGAI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                312 IMDRAGRRLLLIVLSGVVMVFSTSAFGAYFKLTQGGPGNSSHVAISAPVSAQPVDASVGLA
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                                                                                                                                                          434 VLRPYGAFWLASAFCIFSVLFTLFCVPETKGKTLEQITAHF
                                                                                                                                                                                                    446 AWSSGGTFTLYGLVCAFTVVFVTLWVPETKGKTLEELOSLF
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Pred. No. 6.9e-46;
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| DKAGRRLLLTISSVGMTISLVIVAAAFYLKE-
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36.1%;
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Best Local Similarity
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C;Accession: D70073

R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berte C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ch. B.; Bruich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E. Nature 390, 249-256, 1997

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A; Residues: 1-461 <KUN>
A; Rxperimental source: Strain 168
A; Rxperimental source: strain 168
A; Const. Con
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Matches 146; Conservative
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8

Gaps

35;

Length Indels

; Score 606.5; DB 2; ; Pred. No. 2.3e-37; 84; Mismatches 182;

24.7%; 33.7%;

89 81 141

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LVDRAGRKLSLLLCSVPFVAGFAVITAAQDVWMLLGGRLLTGLACGVASLVAPVYISEIA 149
                                                                                                                                                                                                      82 LSFRLGRKYSLMVGAVLFVAGSVGSAFATSVEMLLVARIVLGVAVGIASYTAPLYLSEMA
                                                                                                                                         26 SIAAAVAGLLFGLDIGVIAGALPFITDHFVLSSRLQE----WVVSSMMLGAAIGALFNGW
                                                                                                         30 AFAAALGPLSFGFALGYSSPAIPSLQRAAPPAPRLDDAAASWFGAVVTLGAAAGGVLGGW
                                                       al Similarity 33.7
153; Conservative
                                       Query Match
Best Local S:
Matches 153
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Nature 413, 948-852, 2001

A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serow
A;Reference number: AB0502; MUID:21534947; PMID:11677608
A;Accession: Ab0868
A;Accession: preliminary
A;Molecule type: DAA
A;Residues: 1-471 <PRA>
A;Residues: 1-471 <PRA>
A;Gatus: preliminary
A;Genterics: GB:AL513382; PIDN:CAD02842.1; PID:gl6504096; GSPDB:GN00176
C;Superfamily: allorer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               348 GNSSHVAISAPVSAQPVDASVGLAWLAVGSMCLFIAGFAVGWGPIPWLLMSEIFPLHVKG 407
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           394 FGITCSTTINWVSNMIIGATFLTLLDSIGAAGTFWLYTALNIAFIGITFWLIPETKNVTL 453
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           56 TSRLQE----WVVSSMMLGAAIGALFNGWLSFRLGRKYSLMAGAILFVLGSAFASSV
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                                                                                                                                                                                                                                                                                                                                                                                                ----RRMNMFVSVSAAVAG-LLFGLDIGVIAGALPFITDHFVL
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                                                                                                                                                                                                                                                                                                                               48;
                                                                                                                                                                                                                                                                                            Length 471;
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                                                                                                                                                                                                                                                                                                                             192;
                                                                                                                                                                                                                                                                                          24.7%; Score 607; DB 2; 32.7%; Pred. No. 2.1e-37; ive 85; Mismatches 192
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847089
arabinose-proton symporter - Klebsiella oxytoca
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LTPRSLRDT
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A;Nolecule type: DNA
A;Residues: 1-25, '',349,'R' <RES-
A;Cross-references: EMBL:X00272; NID:g40940; PIDN:CAA25075.1; PID:g40941
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 27, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
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150 YPAVRGLLGSCVQLMVVVGILLAYLAGWVLEW--RWLAVLG--CVPPSLMLLLMCFMPET 205
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C;Species: Bacherichia coll.
C;Date: 05-Oct-1988 #sequence revision 05-Oct-1988 #text_change 01-Mar-2002
C;Accession: B26430; A28075; I40996; B65067
R;Maiden, M.C.J.; Davis, E.O.; Baldwin, S.A.; Moore, D.C.M.; Henderson, P.J.
Nature 325, 441-643, 1987
A;Title: Mammalian and bacterial sugar transport proteins are homologous.
A;Reference number: A93389; MUID:87115869; PMID:3543693
                                          142 SENVRGKMISMYQLMVTLGIVMAFLSDTAFSYSGNWRAMLGVLALPAVVLIILVIFLPNS
                                                                                                                                              PRFLLTQHRRQEAMAALRFLWGSEQGWEDPPIGAEQSFHL----ALLR-QPGIYKPFII
                                                                                                                                                                                               |||:| : | || || || : : || prwlaekgrhveaeevlrmindsekardelneireslkikqggwalfkvnrnvrravfl
                                                                                                                                                                                                                                                                                            260 GVSLMAFQQLSGVNAVMFYAETIFEEAKF---KDSSLASVVVGVIQVLFTAVAALIMDRA
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A;Residues: 1-472 <MA2>
A;Cross-references: GB:J03732; NID:g145320; PIDN:AAA23469.1; PID:g145321
B;Stoner, C.; Schleif, F.
J. Mol. Biol. 171, 369-381, 1983
A;Title: The araE low affinity L-arabinose transport promoter. Cloning, 8
A;Reference number: 140996; MUID:84114868; PMID:6319708
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A,Residues: 1-472 <MAI>
R,Maiden, M.C.J.; Jones-Moxtimer, M.C.; Henderson, P.J.F.
J. Biol. Chem. 263, 8003-8010, 1988
A,Title: The cloning, DNA sequence, and overexpression of the gene araE A,Reference number: A28075; MUID:88228015; PMID:2836407
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   322 GRKPALKIGFSVMAIGTLVLG--YCLMQFDNGT-----
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in

arabinose-proton symport

Cispecies: Klebsishla oxytoca (Species: Klebsishla oxytoca (Species: Klebsishla oxytoca (Species: Man-1995 #sequence\_revision 13-Jan-1995 #text\_change 24-Sep-1999 C;Accession: 847089 #sequence\_revision 13-Jan-1995 #text\_change 24-Sep-1999 C;Accession: 847089 #sequence of the gene araE for arabinose-proton submitted to the EMBL Data Library, June 1994 A;Description: The nucleotide sequence of the gene araE for arabinose-proton A;Reference number: 847089 A;Reference preliminary A;Accession: 847089 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-472 <SHA> A;Cross-references: EMBL:X79598; NID:g498919; PIDN:CAA56110.1; PID:g498920 C;Superfamily: glucose transport protein C;Keywords: arabinose transport

4

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L-arabinose isomerase (EC 5.3.1.4) - Escherichia coli (strain 0157:H7, substrain EDL933 Cispecies: Escherichia coli (cispecies: Escherichia coli (cispecies: Escherichia coli (cispecies: 16-Peb-2001 #sequence_revision 16-Peb-2001 #text_change 31-Dec-2001 Cispeciession: E85336 Riberna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhev Iller, L.; Grotheck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, Nature 409, 529-533, 2001 A; Plunkett Bscherichia coli 0157:H7.
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-472 <STO>
A;Cross-references: GB:AE005174; NID:g12517333; PIDN:AAG57953.1; GSPDB:GN00145; UWGP:Z41
A;Experimental source: strain O157:H7, substrain EDL933
    9
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                                                                                                                                    69 ASWFGAVVILGAAAGGVLGGWLVDRAGRKLSLLLCSVPFVAGFAVITAAQDVWMLLGGRL 128
                                                                                                                                                                 63 --WVVSSMMLGAAIGALFNGWLSFRLGRKYSLMAGAILFVLGSIGSAFATSVEMLIAARV 120
                                                                                                                                                                                                                            LIGLACGVASLVAPVYISEIAYPAVRGLLGSCVQLMVVVGILLAYLAGWVLEW--RWLAV 186
                                                                                                                                                                                                                                                      LG--CVPPSLMLLLMCFMPETPRFLLTQHRRQEAMAALRFLWGSEQGWEDPPIGAEQSFH 244
                                                                                                                                                                                                                                                                                                                                                                                                              L----ALLR-QPGIYKPFIIGVSLMAFQQLSGVNAVMFYAETIFEEAKF---KDSSLAS 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VVVGVIQVLFTAVAALIMDRAGRRLLLVLSGVVMVFSTSAFGAYFKLTQGGPGNSSHVAI 355
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                                          9 TOPLLGPPGGSAPRGRRVFLAAFAAALGPLSFGFALGYSSPAIPSLQRAAPPAPRLDDAA
                                                                                          6 TESALTPRSIRDTRRMNMFVSV-AAAVAGLIFGLDIGVIAGALPFITDHFVLTSRLQE--
                                                                                                                                                                                                                                                                                                                                                                                                                                     241 LKQGGWALFKINRNVRRAVFLGMLLQAMQQFTGMNIIMYYAPRIFKMAGFTTTEQOMIAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SAPVSAQPVDASVGLAWLAVGSMCLFIAGFAVGWGPIPWLLMSEIFPLHVKGVATGICVL
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  36;
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33.3%; Pred. No. 4.1e-37;
ive 84; Mismatches 197; Indels
    Indels
  84; Mismatches 197;
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C,Superfamily: glucose transport protein
C,Keywords: intramolecular oxidoreductase; isomerase
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158; Conservative
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                                                                                                                                                                 A,Map position: 61 min
C,Superfamily: glucose transport protein
C,Keywords: arabinose transport; intramolecular oxidoreductase; isomerase; membrane prot
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C;Date: 18-Ual-2001 #Sequence_revision 18-Jul-2001 #text_change 31-Dec-2001

C;Date: 18-Ual-2001

C;Date: 18-Ual-2001

C;Accession: B91091

R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.

By 11-22, 2001

A;Reference number: Ageloge acuence of enterohemorrhagic Escherichia coli 0157:H7 and genc

A,Reference number: Ageloge; MUD:21156231; PMID:11258796

A,Reference number: Ageloge; MUD:21156231; PMID:11258796

A,Residues: 1-472 cHAY

A,Residues: 1-472 cHAY
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                                                    A;Residues: 1-472 <BLAT>
A;Residues: 0.000368; 0.000368; NID:92367165; PIDN:AAC75880.1; PID:91789207;
A;Experimental source: strain K-12; substrain MG1655
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -- WVVSSMMLGAAIGALFNGWLSFRLGRKYSLMAGAILFVLGSIGSAFATSVEMLIAARV 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VVVGVIQVLFTAVAALIMDRAGRRLLLUVLSGVVMVFSTSAFGAYFKLTQGGPGNSSHVAI 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SAPVSAQPVDASVGLAWLAVGSMCLFIAGFAVGWGPIPWLLMSEIFPLHVKGVATGICVL 415
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         A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                     TQPLLGPPGGSAPRGRRVFLAAFAAALGPLSFGFALGYSSPAIPSLQRAAPPAPRLDDAA
                                                                                                                                                                                                                                                                                                                                                                                                                                          ASWFGAVVTLGAAAGGVLGGWLVDRAGRKLSLLLCSVPFVAGFAVITAAQDVWMLLGGRL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LG--CVPPSLMLLLMCFMPETPRFLLTQHRRQEAMAALRFLWGSEQGWEDPPIGAEQSFH
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                                                                                                                                                                                                                                                                    Length 472;
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                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                             ; Score 603; DB 2; L; Pred. No. 4.1e-37; 84; Mismatches 197;
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C.Superfamily: glucose transport protein
C.Keywords: intramolecular oxidoreductase; isomerase
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Pred. No. 4.1e-37;
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Best Local Similarity 33.3%
Matches 158; Conservative
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Best Local Similarity
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Oy 421 AFLVTKEFSSLMEVLRPYGAFWLASAFCIFSVLFTLFCVPETKGKTLEOITAH-FEGR 477  By NMIVGATFLTMLNTLGNANTFWVAALNVLFTLLTLWLVPETKHVSLEHIERNLMKGR 455  RESULT 10  C31106  Galactose-proton symport of transport system ECs3819 [imported] - Escherichia coli (stra c; pate: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001  C; Accession: C91106  R; Mayashi, T; Maxino, K; Ohnishi, M; Kurokawa, K; Ishii, K; Yokoyama, K; Han, C.G gasawara, N; Yasunaga, T; Kuhara, S; Shiba, T; Hattori, M; Shinagawa, H. DNA Res. 8, 11-22, 2001  A; Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gend A; Reference number: A99629; MUID:21156231; PMID:11258796  A; Residues: 17-64 < AAX > A; Cross-references: GB:BA000007; PIDN:BAB37242.1; PID:g13362291; GSPDB:GN00154  A; Experimental source: strain O157:H7, substrain RIMD 0509952  C; Genetics: A; Genes Ersanport protein	Query Match   23.9%;     Best Local Similarity   32.2%;     Matches   154;   Conservative   6     Qy   27   FLAAFAAALGPISFGFALG                         Db   16   FVCFLAALAGLEGLDICS     Qy   R7   GGMLVDRAGRKLSILLCS     Qy   147   EIAYPAVRGLIGSCYQLM     Db   132   EIAPERIRGSMISMYQLM     Db   132   EIAPERIRGSMISMYQLM     Db   245   LALLROPGIYKPFI - IGW     Qy   245   LALLROPGIYKPFI - IGW     Db   240 - ALFKENSNFRAVFLGWI     Db   240 - ALFKENSNFRAVFLGWI     Db   299   TWULATFIAGLUDRWGRM     Qy   361   AQPVDASVGLAMLANGSM     Qy   347   AQYFALAMLI     Db   347   AQYFALAMLI     Db   347   AQYFALAMLI     Db   348   NMIVGATFLIMLNTIGNAN	RESULT 11 F8551 galactose-proton symport of transport system [imported] - Escherichia coli (strain O157 galactose-proton symport of transport system [imported] - Escherichia coli (\$2000 c; \$2000 c; \$20
OY 187 LGCVPPSLMLLIMCFMPETPRFLLTQHRRQEAMAALRFLWGSEQGWEDPPIGAEGSFH 244  Db 181 LGVLALPAVLLIILVVFLPNSPRWLAEKGRHIEAEEVLRMLRDTSEKAREELNEIRESLK 240  OY 245 LALLR-OPGIYKPFIIGVSLWAFQOLSGVNAVMFYAETIFEBAKFKDSSLAS 295  241 LKQGGWALFKINRNVRRAVFLGMLLOAMQOFTGWNIIMYYAPRIFKWAGFTTTEQQMIAT 300  OY 296 VVVGVIQVLFTAVAALIMDRAGRRLLLVLSGVNAVFSTSAFGAYFKLTQGGFGNSSHVAI 355	Cincession: F65079 A: Rosesion: F65079 A: Rose, D. J. Mau, B.; Shao, Y. Science 277, 1433-4462, 1997 A: flose, D. J. Mau, B.; Shao, Y. Science 277, 1433-4462, 1997 A: flose 277 A: flose 278 A: flos	Db 240 -ALFKENSNFRRAVEIGHILOVMQFTGNNVIMYYAPKIFELAGYTNTFEGMWGTVIVGL 298  QY 301 IQVLFTAVAALIMDRAGRRILLVIGGVMVFSTSAFGAYFKLTGGGFONSSHVAISAPVS 360  Db 299 TNVLATFIAIGLVDRWGRKPTLTLGFLVMAAGMGVLGTWMHIGHSP-S 346  QY 361 AQPVDASVGLAMLAVGSMCLFIAGFAVGWGPIPWLLMSEIFPLHVKGVATGICVLTNWLM 420  Bb 347 AQYFAIAMLLMFIVGFAMGAGPLIWVLCSEIQPLKGRDFGITCSTATNWLM 397

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A,Molecule type: DNA
A,Residues: 290-575 <GEN>
A,Cross-references: EMBL:299532; PIDN:CAB16718.1; GSPDB:GN00066; SPDB:SPAC7D4.01
A,Experimental source: strain 972h-; cosmid c7D4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RYAYPLIIGVGLMELQQLCGSSGVTYYASSLFNKGGF-PSAIGTSVIATIMVPKAMLATV 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 312 IMDRAGRRILLVLSGVVMVFST-----SAFGAYFKLTQGGPGNSSHVAISAPVSAQ 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        388
                                                                                                                                   LGGWLVDRAGRKLSLLLCSVPFVAGFAVITAAQDVWMLLGGRLLTGLACGVASLVAPVYI 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PVDASVGLAWLAVGSMCLFIAGFAVGWGPIPWLLMSEIFPLHVKGVATGICVLTNWLMAF 422
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Cispecies: Schizosaccharomyces pombe
Cipate: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 20-Oct-2000
Cipate: 21-Jan-3400; T39079
Rividerberger, C.
Rividerberger, C.
A;Reference number: 22484
A;Reference number: 22484
A;Reference number: 225484
A;Rocession: T43400
A;Rolecule type: DNA
A;Rosidues: 1-575 ANIE>
A;Cross-references: EMBL: X98622; PIDN: CAA67211.1
A;Experimental source: strain 968 H90
B;Gentles, S; Churcher, C.M.; Wood, V.; Barrell, B.G.; Rajandream, M.A.
Subfaced C. C.M.; Rolecule Library, September 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             441 IITYTFNFMLE------WNASGMFLIFSMVSASSIVFIYFLVPETKGRSLEEIQA 489
                                                                                                                                                                                                                                                                                               VFLAAFAAALGPLSFGFALGYSSPAIPSLQRAAPPAPRLDDAAASWFGAVVTLGAAAGGV
                                                        SEIAYPAVRGLLGSCVQLMVVVGILLAYLAGWVLEWRWLAVLGCVPPSLMLLLMCFMPET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             114 FSGKVADVLGRKRTMLFCEFFCITGWLCVALAQNAMWLDCGRLLLGIGVGIFSYVIPVYI
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                                                                                                                                                                                                                                                                                                                                                                             PRFLLTQHRRQEAMAALRFLWGSEQGWEDPPIGAEQS-
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C;Superfamily: maltose transport protein MAL61
C;Keywords: sugar transport; transmembrane protein
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Best Local Similarity 29.84
Matches 147; Conservative
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A, Accession: T39079
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                                                     A;Accession: Fessa.
A;Status: preliminary
A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-464 <STO>
A;Cross-references: GB:AE005174; NID:g12517486; PIDN:AAG58074.1; GSPDB:GN00145; UMGP:242
A;Experimental source: strain 0157:H7, substrain EDL933
C;Genetics:
A;Genetics:
A;Genet
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R;Kiyosue, T.; Abe, H.; Yamaguchi-Shinozaki, K.; Shinozaki, K.
Biochim. Biophys. Acta 1370, 187-191, 1998
A;Title: ERD6, a cDNA clone for an early dehydration-induced gene of Arabidopsis, encode
A;Reference number: Z25973; MUID:98213606; PMID:9545564
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
Title: Genome sequence of enterohemorrhagic Escherichia coli 0157:H7. Reference number: A85480; MUID:21074935; PMID:11206551
                                                                                                                                                                                                                                                                                                                                                                                                                               65;
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                                                                                                                                                                                                                                                                                                                                                             Query Match
23.9%; Score 587.5; DB 2;
Best Local Similarity 32.2%; Pred. No. 5.6e-36;
Matches 154; Conservative 83; Mismatches 176;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;Keywords: transmembrane protein; transport protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Accession: T52132
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
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A;Cross-references: EMBL:D89051; PIDN:BAA25989.1
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Db 240 -ALFKENSNFRRAVFLGILLQVMQOFTGMNVIMYYAPKIFELAGYTNTTEQMMGTVUVGL 298  Qy 301 IQVLFTAVALIMDRAGRRLLLVLSGVVMVFSTSAFGAYFKLTQGGPGNSSHVAISAPVS 360	RESULT 15  G84864 probable membrane transporter [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ar cress) C;Species: Arabidopsis thaliana (mouse-ar cress) C;Species: Arabidopsis thaliana (mouse-ar cress) C;Date: O2-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001 C;Accession: G84864 R;iin, X; Kaul, S; Rounsley, S.D; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; K;iin, X; Kaul, S; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; K;iin, X; Kaul, S; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M;ithe: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A;Reference number: A84420; MUID:20083487; PMID:10617197 A;Reference number: A84420; MUID:20083487; PMID:10617197 A;Reference number: A84420; MUID:20083487; PMID:10617197 A;Reference: 1521 egro. A;Gratus: preliminary A;Molecule type: DNA A;Grastreferences: GB:AE002093; NID:g2289003; PIDN:AAB64332.1; GSPDB:GN00139 C;Genetics: A;Genetics: A;Genetics: C;Guetics: C;Guetics	OWERY MATCH  23.7%; Score 582; DB 2; Length 521;  Best Local Similarity 31.0%; Pred. No. 1.6e-15;  Matches 147; Conservative 76; Mismatches 191; Indels 60; Gaps 9;  Qy 33.AalGelesGredaries
OY 125 GGRLLTGLACGVASLVAPVYISEIAYPAVRGLLGSCVQLMVVVGILLAYLAGWVLE 180  185 VGRFVIGWGVGIASLIIPLYLSEIAPSKIRGRLVIIYVLLITAGOVIAYGIDTAFEHVHN 244  181 -WRWLAVLGCVPPSLMLLLMCFMPETPRFLLTQHRRQEAMAALRFLWGS 228  181 -WRWLAVLGCVPPSLMLLMCFMPETPRFLLTQHRRQEAMAALRFLWGS 228  245 GWRWWYGLAMVPRAFQLFILIWLPESPRLLVGHRQEAMAALRFLWGS 228  QY 229EQGWEDPPIGAEQSFHLALLRQPGIYKPFIIGVSLMAFQQLSGVNAVMFYAET 281  DD 305 LIQEGVRDPFSGSRWQKIYKTFK-ELYFNPSNFRALILACGLQAMQQLSGFNSLMYFSST 363  282 IFBEAKFKOSSLASVVVGVIQVLFFTAVAALIMDRAGRRLLLVLSGVVWWFSTSAFGAY 339  QY 18EVVGFNNPTATGLIIAATNFVFTIVAFGVIDFFGRRILLLLTVWGMIAALIVCAVAFF 423	PIPWLLM 397 :     NLFW-OO 467 SVLFTLF 457         GWLGALF 527 GWLGALF - Salmonel NOV-2002 ; Wain, J.;	

Search completed: September 27, 2004, 19:30:11 Job time : 51 secs

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GenCore version 5.1.6
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- protein search, using sw model OM protein September 27, 2004, 19:09:21 ; Search time 25 Seconds
(without alignments)
993.499 Million cell updates/sec Run on:

US-09-886-954A-1 2457 1 MTPEDPEETQPLLGPPGGSA......CVPETKGKTLEQITAHFEGR 477 Title:

Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

141681 seqs, 52070155 residues Searched: 141681 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_42:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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GTR1_MOUSE	ITR1_YEAST	GTR1 BOVIN	GTR1 HUMAN	GTR1 RAT	GTR2 HUMAN	GTR1 CHICK	ITR2_SCHPO	GTR1 RABIT	GTR3 RABIT	GLF ZYMMO	GTRZ_CHICK
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## ALIGNMENTS

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TISSUE=Testis;
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                                                                                                                                                                                                                       PROSITE; PS50850; MFS; 1.
PROSITE; PS00216; SUGAR_TRANSPORT_1; 2.
PROSITE; PS00217; SUGAR_TRANSPORT_2; 1.
Transport; Sugar transport; Transmembrane; Glycoprotein; Multigene family.
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GO:0005355; F:glucose transporter activity; TAS. GO:0005975; P:carbohydrate metabolism; TAS. GO:0015758; P:glucose transport; TAS.
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InterPro; IPR005828; Sub_transporter.
InterPro; IPR005829; Sug_transporter.
InterPro; IPR005829; Sug_transporter.
InterPro; IPR00363; Sugar_tr; I.
Prints; Pr00083; Sugar_tr; I.
PRINTS; PR00171; SUGRIRNSPORT.
IIGREAMS; IIGR00899; SP; I.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
420
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                                                                                                                                                                                                        477
                                                                                                                                                                                                                                           421 AFLVTKEFSSLMEVLRPYGAFWLASAFCIFSVLFTFSCVPETKGKTLEQITAHFEGR 477
                                                                                 361 AQPVDASVGLAWLAVGSMCLFIAGFAVGWGPIPWLLMSEIFPLHVKGVATGICVLTNWLM
                                                                                                                         SUBCELULIAR LOCATION: Integral membrane protein. Principally intracellular. May move between intracellular vesicles and the plasma membrane. The dileucine internalization motif is critical for intracellular sequestration.

TISSUE SPECIFICITY: Highly expressed in adult and pubertal testis, but not prepubertal testis. Moderate expression in hypothalamus, but not prepubertal tistis. Moderate expression in hypothalamus, amounts present in most other tissues.

SIMILARITY: BELONGS TO THE SUGAR TRANSPORTER FAMILY. GLUCOSE TRANSPORTERS SUBFAMILY.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Molecular cloning of a new putative glucose transporter."; Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A., CHARACTERIZATION, AND MUTAGENESIS OF
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SAQPVDASVGLAWLAVGSMCLFIAGFAVGWGPIPWLLMSEIFPLHVKGVATGICVLTNWL 419
                                                                                                                                                                                                                                                                                                                  Biol. Chem. 275:16275-16280(2000)
                                                                                                                                                                                                                                                                         TISSUE=Testis;
MEDLINE=20283667; PubMed=10821868;
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CHANGES SUBCELLULAR LOCATION
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DILEUCINE INTERNALIZATION MOTIF
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                                                                                   Sugar transport; Transmembrane; Glycoprotein;
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LL->AA: C
       InterPro; IPR005828, Sub_transporter.
InterPro; IPR005829; Sug_transporter.
InterPro; IPR003663; Sugar_transpt.
                                                           PROSITE; PS50850; MFS; 1.
PROSITE; PS00216; SUGAR_TRANSPORT_1;
PROSITE; PS00217; SUGAR_TRANSPORT_2;
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                                Pfam; PF00083; sugar tr; 1.
PRINTS; PR00171; SUGRIRNSPORT.
TIGREAMS; TIGR00879; SP; 1.
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  InterPro; IPR007114; MFS
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361 SAEPADVHLGLAWLAVGSMCLFIAGFAVGWGPIPWLLMSEIFPLHIKGVATGVCVLTNWF 420
                                                                               420 MAFLVTKEFSSLMEVLRPYGAFWLASAFCIFSVLFTLFCVPETKGKTLEQITAHFEGR 477
                                                                                                                                    421 MAFLVTKEFNSIMEIIRPYGAFWLTAAFCILSVLFTLTFVPETKGRTLEQITAHFEGR 478
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TISSUE SPECIFICTTY: Highest level of expression in placenta and restis. Highly expressed in adult and pubertal testis, but not prepubertal testis. Lower levels of expression in brain, liver, heart, kidney, fat and skeletal muscle.

BEWILOPMENTAL STAGE: High expression in blastocysts.

INDUCTION: Inhibited under glucose deprivation.

SIMILARITY: BELONGS TO THE SUGAR TRANSPORTER FAMILY. GLUCOSE TRANSPORTERS SUBFAMILY.
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MEDLINE=20319023; PubMed=10860996;
Carayannopoulos M.O., Chi M.M.-Y., Cui Y., Pingsterhaus J.M.,
McKnight R.A., Mueckler M., Devaskar S.U., Moley K.H.;
"GLUTB is a glucose transporter responsible for insulin-stimulated
glucose uptake in the blastocyst.";
Proc. Natl. Acad. Sci. U.S.A. 97:7313-7318 (2000).
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MEDLINE=21547794; PubMed=11689004;
Scheepers A., Doege H., Joost H.-G., Schuermann A.;
"Mouse GLUT8: genomic organization and regulation of expression in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seems to
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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-!- FUNCTION: Insulin-regulated facilitative glucose transporter.
Binds cytochalasin B in a glucose-inhibitable manner. Seems to a dual-specific sugar transporter as it is inhibitable by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        member
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=20138191; PubMed=10671487; Ibberson M.R., Uldry M.A., Thorens B.; GLUTL, a novel mammalian glucose transporter expressed in the central nervous system and insulin-sensitive tissues."; J. Biol. Chem. 275:4607-4612(2000).
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                                                                                                                                                                                                                                                                                                                                                                          GTR8 MOUSE SIAMULE.

Q9JIF3; O9JIP4; Q9JUZQ;

Q9JIF3; O9JUP4; Q9JUZQ;

28-FEB-2003 (Rel. 41, Last sequence update)

28-FEB-2003 (Rel. 41, Last annotation update)

28-FEB-2003 (Rel. 41, Last annotation update)

Solute carrier family 2, facilitated glucose transporter, m

(Glucose transporter type 8) (Glucose transporter type XI).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-LINKED (GLCNAC. . .) (By similarity)
S -> N (IN REF. 1).
S -> A (IN REF. 2 AND 4).
S -> N (IN REF. 1).
A3753FB34E452F9A CRC64,
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CYTOPLASMIC (POTENTIAL).
DILEGCINE INTERNALIZATION MOTIF (BY
SIMILARITY).
                                                                                                 EMBL; AJ245936; CABB9815.1; -.

R EMBL; AJ245936; CABB9815.1; -.

R EMBL; AJ413951; CAC88690.1; -.

R EMBL; AJ413951; CAC88690.1; -.

R MGD; MGI:L860103; S1C2A8.

GO; GO:0005887; C:integral to plasma membrane; IDA.

R GO; GO:0005887; C:integral to plasma membrane; IDA.

R GO; GO:0005887; P:glucose transporter activity; IDA.

R GO; GO:0005355; F:glucose transporter activity; IDA.

R GO; GO:00016758; P:glucose transport; IDA.

R GO; GO:0001666; P:response to hypoxia; IDA.
                                                                                                                                                                                                                                                                                                                             PROSITE; PS50850; MFS; 1.
PROSITE; PS00216; SUGAR TRANSPORT 1; 1.
PROSITE; PS00217; SUGAR TRANSPORT 2; 1.
Transport; Sugar transport; Transmembrane; Glycoprotein;
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EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
10 (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
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InterPro; IPR005829; Sug_transporter.
InterPro; IPR003663; Sugar_transpt.
Pfam; PF00083; Bugar_tr; 1.
PRINTS; PR00171; SUGRTRNS-DRT.
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2; 9 9 1 MIPEDPEETQPLLGPPGGSAPRGRRVFLAAFAAALGPLSFGFALGYSSPAIPSLQRAAPP 2; 87.7%; Score 2156; DB 1; Length 477; 86.0%; Pred. No. 3e-144; iive 31; Mismatches 34; Indels 2 Conservative Local Similarity nes 411; Conserv Query Match Best Loca Matches

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EMBL; AF321324; AAK69606.1; -. InterPro; IPR007114; MFS.

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                     121 WMLIGGRILIGLACGVASLVAPVYISEIAYPAVRGLIGSCVOLMVVTGILLAYVAGWVLE
APRLDDAAASWFGAVVTLGAAAGGVLGGWLVDRAGRKLSLLLCSVPFVAGFAVITAAQDV
                                                                             WMLLGGRLLTGLACGVASLVAPVYISEIAYPAVRGLLGSCVQLMVVVGILLAYLAGWVLE
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
50lute carrier family 2, facilitated glucose transporter, member 8
Glucose transporter type 8) (Glucose transporter type XI) (Fragment).
SLC2A8 OR GLUT8 OR GLUTX1.
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SUBCELLULAR LOCATION: Integral membrane protein. Principally intracellular. May move between intracellular vesicles and the plasma membrane. The dileucine internalization motif is critical for intracellular sequestration (By similarity).
SIMILARITY: BELONGS TO THE SUGAR TRANSPORTER FAMILY. GLUCOSE
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Mol. Reprod. Dev. 60:370-376(2001).
-!- FUNCTION: Insulin-regulated facilitative glucose transporter.
Binds cytochalasin B in a glucose-inhibitable manner. Seems to
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
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BEDLINE-1482567; PubMed=11599048;
Augustin R., Pocar P., Navarrete-Santos A., Wrenzycki C.,
Niemarn H., Fischer B.;
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Pred. No. 5.4e-101;
17; Mismatches 23; Indels 1;
                                                                                                                                                                                                          Transport; Sugar transport; Transmembrane; Multigene family.

NON TER 1 1 CYTOPLASMIC (POTENTIAL).
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28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Solute carrier family 2, facilitated glucose transporter,
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SLC2A6 OR GLUT9.
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EXTRACELLULAR (POTENTIAL).
8 (POTENTIAL).
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9 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
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0EE9B670ADAB71DD CRC64;
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CYTOPLASMIC (POTENTIAL)
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PROSITE; PS00216; SUGAR TRANSPORT 1; 1.
PROSITE; PS00217; SUGAR_TRANSPORT_2; PARTIAL.
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InterPro; IPR005828; Sub_transporter.
InterPro; IPR005829; Sug_transporter.
Pfam; PF00083; sugar tr; 1.
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                                                                                                                                                                                                                                                                                                                                                 A Straubberg R.L., Feingdel E.A., Grouse D.H., Derge J.G.,

Straubberg R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jozdan H., Moore T., Max S.I., Wang J., Hsieh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Richards S.W., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S.W., Worley K.C., Hale S., Garcia A.M., Gabbs R.A.,

Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Paley J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.M., Krzywinski M.I., Skalska U., Smailus D.E.,

Roberstion and initial analysis of more than 15,000 full-length

Human and mouse Colls.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (By similarity).
TISSUE SPECIFICITY: Highly expressed in brain, spleen and peripheral blood leukocytes.
SIMILARITY: BELONGS TO THE SUGAR TRANSPORTER FAMILY. GLUCOSE TRANSPORTERS SUBFAMILY.
TRANSPORTERS SUBFAMILY.
CAUTION: Has been described as GLUT9 in litterature, but this gene name has already been used for SLC2A9.
Doege H., Bocianski A., Joost H.-G., Schuermann A.;
"Activity and genomic organization of human glucose transporter 9 (GLOT9), a novel member of the family of sugar-transport facilitators predominantly expressed in brain and leucocytes.";
Biochem. J. 350:771-776 (2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'Cloning of a sugar transporter gene, a G-beta subunit like gene and three novel genes in human chromosome 9q34."; submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                         TISSUE=Lymphoid;
Young J.M., Woodward K.J., Aziz S., Burley M., Kwiatkowski D.J.,
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InterPro; IPR005829; Sug_transporter.
InterPro; IPR003663; Sugar_transpt
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EMBL; BC013740; AAH13740.1; -.
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MIM; 606813;
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PS00216; SUGAR\_TRANSPORT\_1; 1. PS00217; SUGAR\_TRANSPORT\_2; 1.

PROSITE; PS50850; MFS; 1. PROSITE; PS00216; SUGAR 7 PROSITE; PS00217; SUGAR 7

SUGRIRNSPORT.

Pfam, PF00083, sugar tr; 1. PRINTS, PR00171, SUGRTRNSPOI TIGRFAMS, TIGR00879, SP; 1.

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CSBC_BACSU
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This SWISS-PROT entry is copyright. It is produced through a collaboration
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                                                                                                                                                                                                                                                                                                                        MEDLINE=96093926; PubMed=7584049;
Yoshida K.-I., Seki S., Fujimura M., Miwa Y., Fujita Y.,
Cloning and sequencing of a 36-kb region of the Bacillus subtilis
genome between the gnt and iol operons.";
DNA Res. 2:61-69(1995).
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-!- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
-!- SIMILARITY: Belongs to the sugar transporter family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=99303315; PubMed=10376822;
Akbar S., Lee S.Y., Boylan S.A., Price C.W.;
"Two genes from Bacillus subtilis under the sole control of t
general stress transcripting factor sigmaB.";
Microbiology 145:1069-1078(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Yoshida K.-I.;
                                                                                                                                                                                                       Firmicutes; Bacillales; Bacillaceae; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fujita Y., Shibayama T., Ishio I., Aoyama D., Yoshida K.
Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
CSBC_BACSU STANDARD; PRT; 461 AA. P4633BC_BACSU STANDARD; PRT; 461 AA. P4633B, 0322BS (Rel. 32, Created) 10-0CT-2003 (Rel. 42, Last sequence update) 110-CCT-2003 (Rel. 42, Last annotation update) Probable metabolite transport protein csbC. CSBC OR SSS2BR OR BSU338B10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=98044033; PubMed=9384377;
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STRAIN=168 / BGSC1A1;
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between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24.7%; Score 607; DB 1; Length 46 31.1%; Pred. No. 1.5e-35; ive 85; Mismatches 192; Indels
                                                                                                                                                                                                                                           1 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                         TIGREAMS; TIGRO0879; SP; 1.
PROSITE; PS50850; MFS; 1.
PROSITE; PS00216; SUGAR_TRANSPORT_1; 2.
PROSITE; PS00217; SUGAR_TRANSPORT_2; 1.
Transport; Transmembrane; Complete proteome.

Transport; Transmembrane; Complete proteome.
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EXTRACELLULAR (POTENTIAL)
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EXTRACELLULAR (POTENTIAL)
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EXTRACELLULAR (POTENTIAL)
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AD59CB5DD6372FE0 CRC64;
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EXTRACELLULAR (POTENTIAL)
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                                                                                                  Subtlist; BG11360; csbC.
InterPro; IRR007114; MFG.
InterPro; IRR005828; Sub_transporter.
InterPro; IRR005828; Sug_transporter.
InterPro; IRR003663; Sugar_transpt.
Pfam; Pro00881; sugar_trin.
PRINTS; PR00171; SUGRTRNSPORT.
IIGREAMS; IIGR00879; SP; 1.
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                                                                     EMBL; AB005554; BAA21604.1; -.
EMBL; Z99124; CAB16017.1; -.
PIR; D70073; D70073.
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461 AA;
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 AALIMDRAGRRLLLVLSGVVMVFSTSAFGAYFKLTQGGPGNSSHVAISAPVSAQPVDASV 368
                                   ---LSA 335
                                                                    428
                                                                                             STAWMTVVFLGVYIVFYQATWGPVVWVLMPELFPSKARGAATGFTTLVLSAANLIVSLVF
                                                               GLAWLAVGSMCLFIAGFAVGWGPIPWLLMSEIFPLHVKGVATGICVLTNWLMAFLVTKEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the concomitant export of a proton (symport system).
SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane.
SIMILARITY: Belongs to the sugar transporter family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Shatwell K.P., Charalambous B.M., McDonald T.P., Henderson P.J.F.; "Cloning, sequencing, and expression of the araB gene of Klebsiella oxytoca 8017, which encodes arabinose-H+ symport activity."; J. Bacteriol. 177:5379-5380(1995).
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PROSITE; PS00216; SUGAR_TRANSPORT_1; 1.

PROSITE; PS00217; SUGAR_TRANSPORT_2; 1.

Transport; Sugar transport; Transmembrane; Inner membrane; Symport.

DOMALN 1 29 CYPOPLASMIC (POTENTIAL).

TRANSMEM 30 50 1 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Klebsiella.
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                                                                                                                                                           396 PLMLSAMGIAWVFMVFSVIČLLŠFFFAFYMVPETKGKSLEEIEASLKKR 444
                                                                                                                               SSIMEVLRPYGAFWLASAFCIFSVLFTLFCVPETKGKTLEQITAHFEGR
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5 (POTENTIAL)
PERIPLASMIC (POTENTIAL).
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PERIPLASMIC (POTENTIAL)
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CYTOPLASMIC (POTENTIAL)
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4 (POTENTIAL).
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28-FEB-2003 (Rel. 41, Last annotation update)
Arabinose-proton symporter (Arabinose transporter).
                    472 AA
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InterPro; IPR005829; Sug_transporter.
InterPro; IPR013631; Sugar_transpt.
Pfan; PF00183; sugar_tr; 1.
PRINTS; PR00171; SUGRIFNSPORT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=8017;
MEDLINE=95394866; PubMed=7665532;
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01-NOV-1995 (Rel. 32, Last seq
28-FEB-2003 (Rel. 41, Last ann
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InterPro; IPR007114; MFS.
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InterPro; IPR007114; MFS.
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                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Maiden M.C.J., Davis B.O., Baldwin S.A., Moore D.C.M.,
Henderson P.J.F.;
"Mammalian and bacterial sugar transport proteins are homologous.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Escherichia coli O157:H7.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                   35;
                                                                                                                                              ; Score 606.5; DB 1; Length 472; Pred. No. 1.7e-35; 84; Mismatches 182; Indels 35
                                                                                                                             410021E1BEE3D96E CRC64;
                                                                              (POTENTIAL).
                                                                                                (POTENTIAL).
          7 (POTENTIAL).
PERIPLASMIC (POTENTIAL).
8 (POTENTIAL).
                                                           PERIPLASMIC (POTENTIAL).
  (POTENTIAL)
                                       CYTOPLASMIC (POTENTIAL)
                                                                                                          (POTENTIAL).
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orter (Arabinose transporter).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              437 PYGAFWLASAFCIFSVLFTLFCVPETKGKTLEQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 472 AA
                                                                     10 (POTENTIAL)
                                                                                       11 (POTENTIAL)
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                                                9 (POTENTIAL)
 CYTOPLASMIC
                                                                              CYTOPLASMIC
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                                                                                                 PERIPLASMIC
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ARAE OR B2841 OR 24161 OR ECS3698.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Enterobacteriaceae; Escherichia.
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01-MAR-1989 (Rel. 10, Created)
01-MAR-1989 (Rel. 10, last seque)
28-FEB-2003 (Rel. 41, Last ann
                                                                                                                            51732 MW;
                                                                                                                                               24.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nature 325:641-643(1987).
                                                                                                                                                                   Matches 153; Conservative
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                                                                                                                             472 AA;
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                                                                                                                                                         Similarity
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TRANSMEM
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DOMAIN
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SEQUENCE FROM N.A.
MEDLINE=21156231; PubMed=11258796;
MEDLINE=21156231; PubMed=11258796;
Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
Kuhara S., Shiba T., Hattori M., Shinagawa H.;
"Complete ganome sequence of enterchemorrhagic Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7. Mol. Biol. 171:369-381(1983).
-!- FUNCTION: Uptake of arabinose across the boundary membrane with the concomitant export of a proton (symport system).
-! The concomitant export of a proton (symport system).
-!- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane.
-!- SIMILARITY: Belongs to the sugar transporter family.
                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=K12 / MG1655;
MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Genome sequence of enterohaemorrhagic Escherichia coli 0157:H7."; Nature 409:529-533(2001).
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STRAIN=0157.H7 / EDL933 / ATCC 700927;

MEDLINE=21074935, PubMed=11206551;

Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,

Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,

Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,

Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,

Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,

Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,

Welch R.A., Blattner F.R.,
                                        STRAIN=K12 / JM2433;
MEDLINE=88228015; PubMed=2836407;
Maiden M.C.J., Jones-Mortimer M.C., Henderson P.J.F.;
Maiden M.C.J., Jones-Mortimer M.O. verexpression of the gene arabite cloning, DNA sequence, and overexpression of the gene arabicoging for arabinose-proton symport in Escherichia coli K12.";
J. Biol. Chem. 263:8003-8010(1988).
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Stoner C., Schleif R.F.;
"The araE low affinity L-arabinose transport promoter. Cloning,
sequence, transcription start site and DNA binding sites of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
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J. Mol. Biol. 171:369-3
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PIR, B91091; B91091.
PIR; E85936; E85936.
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FROM N.A
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us-09-886-954a-1.rsp

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-22388234; PubMed-12471157;
Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,
Mayhew G.F., Rose D.J., Jhou S., Schwartz D.C., Perna N.T.,
Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
"Extransive mosaic structure revealed by the complete genome sequence
of uropathogenic Escherichia coli.";
Proc. Natl. Acad. Sci. US.A. 99:17020-17024(2002).
-!- FUNCTION: UPTAKE OF GALACTOSE ACROSS THE BOUNDARY MEMBRANE WITH
THE CONCOMITANT EXPORT OF A PROTON (SYMPORT SYSTEM).
-!- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane.
-!- SIMILARITY: Belongs to the sugar transporter family.
   403 TNWVSNMIIGATFLTLLDSIGAAGTFWLYTALNIAFVGITFWLIPETKNVTLEHI 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS50850; MFS; 1.
PROSITE; PS00216; SUGAR_TRANSPORT_1; 1.
PROSITE; PS00217; SUGAR_TRANSPORT_2; 1.
Transport; Sugar transport; Transmembrane; Inner membrane; Symport;
COMPLETE proteome. 1. CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=K12 / MG1655;
MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V. Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                                                                                 Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                         "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
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                                                                                                       01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Galactose-proton symporter (Galactose transporter).
GALP OR B2943 OR C3529.
Escherichia coli, and
Escherichia coli, and
                                                                                                                                                                                                                                                                                    Roberts P.E.;
Thesis (1992), University of Cambridge, U.K.
                                                                              464 AA
                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A., AND CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entities requires a license agreement (9 or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Enders, Ed12148; galp.
InterPro; IPR007114; MFS.
InterPro; IPR005828; Sub_transporter.
InterPro; IPR005829; Sug_transporter.
InterPro; IPR00563; Sugar_transporter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; AE000377; AAC75980.1; -.; AE016766; AAN81977.1; ALT_INIT.
F65079; F65079.
                                                                                                                                                                                                                             Enterobacteriaceae; Escherichia
NCBI_TaxID=562, 217992;
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                                                                            STANDARD;
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                                                                                         P370<u>2</u>1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        129 LTGLACGVASLVAPVYISEIAYPAVRGLLGSCVQLMVVVGILLAYLAGWVLEW--RWLAV 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LG--CVPPSLMLLLMCFMPETPRFLLTQHRRQEAMAALRFLWGSEQGWEDPPIGAEQSFH 244
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                                                                                    PROSITE; PS50850; MrS; 1. ...
PROSITE; PS00216; SUGAR_TRANSPORT_1; 1.
PROSITE; PS00217; SUGAR_TRANSPORT_2; 1.
Transport; Sugar_transport; Transmembrane; Symport;
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411990A441D44393 CRC64;
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CYTOPLASMIC (POTENTIAL).
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InterPro; IPR005828; Sub_transporter.
InterPro; IPR005829; Sug_transporter.
InterPro; IPR00363; Sugar_transpt.
Pfam; PF00083; sugar_tr; 1.
Pfam; PR00171; SUGRTRNSPORT.
TIGRFAMs; TIGR00879; SP; 1.
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51684 MW;
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472 AA;
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158; Conserv
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                                                                                                                                                                                                                                                                                                        65;
                                                                                                                                                                                                                                                                                 Score 591.5; DB 1; Length 464;
Pred. No. 1.8e-34;
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                                                                                                                                                                                                                                                                                                      83; Mismatches 175; Indels
                                                                                                                                                                                                                                                            07E08935BD8E3F8E CRC64;
                     2 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
MyO-inositol transporter 1.
ITRL OR SPACAF8.15 OR SPAC7D4.01.
Schizosaccharomyces pombe (Fission yeast).

OS CE DATE OF CONTROL OF CONTROL

575 AA

STANDARD;

ITR1 SCHPO Q10286;

ITR1\_SCHPO

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RAY MEDIANS=21844401; PubMed=11859360;
RAY MEDIANS=21844401; PubMed=11859360;
RA Sgouros U., Gavilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A., Ragouros U., Peat N., Hayles J., Basham D., Bowman S., Ray Brooks K., Brown D., Erown S., Chillingworth T., Churcher C.M., RA Gentles S., Goble A., Hamilin N., Harris D., Hidalgo J., Hodgson G., Ray Horrsby T., Howarth S., Huckle B.J., Hunt S., Jagels K., Ames K., Jones L., Jones M., Leather S., McDonald S., McLean J., RA Holroyd S., Morles E., Murphy L., Niblett D., Oddell C., RA James K., O'Neil S., Mnagall K., Murphy L., Niblett D., Oddell C., RA Rabelton J., Simmonds M., Squares R., Squares R., Stevens K., Stevens K., Stevens K., Autherford K., Taylor R.G., Yarley A., Walsh S.V., Warren T., Whitehead S., Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B., Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B., Reger P., Zinmermann W., Wedler H., Reinhardt R., Purnelle B., Rager P., Zinmermann W., Wedler H., Reinhardt R., Purnelle S., Lorado L., Dreano S., Gloux S., Lelaure V., Motter S.M. Locas M., Cadieu E., Dreano S., Gloux S., Lelaure V., Motter S.M. Daga R.R., Cruzado L., Jimenz S., Arnstrong J., Forsburg S.L., Certttil., Lowe T., McCombie W.R., Paulsen I., Potashkin J., M. Pappakovski G.V., Ussery D., Barrell B.G., Nurse P., Nurse P., The Grone Requence of Schizosaccharomyces pombe.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                  STRAIN=968 h90;
MIDLINE-9882828265; PubMed=9560432;
Niederberger C., Graub R., Schweingruber A.-M., Fankhauser H.,
Rusu M., Poitelea M., Edenharter L., Schweingruber M.E.;
Exogenous inositol and genese responsible for inositol transport ar required for mating and sporulation in Shizosaccharomyces pombe.";
Curr. Genet. 33:255-261(1998).
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GO:0007151; P:sporulation (sensu Saccharomyces); ISS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SUBCELLULAR LOCATION: Integral membrane protein. -!- SIMILARITY: Belongs to the sugar transporter family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GeneDB_SPombe; SPAC4F8.15; -. GO; GO:0000747; P:conjugation with cellular fusion; ISS. GO; GO:0006629; P:lipid_metabolism; ISS.
Eukaryota, Fungi, Ascomycota, Schizosaccharomycetes,
Schizosaccharomycetales, Schizosaccharomycetaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- FUNCTION: TRANSPORTER FOR MYO-INOSITOL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR007114; MFS.
InterPro; IPR005829; Sub transporter.
InterPro; IPR005829; Sugar transporter.
InterPro; IPR003663; Sugar transpt.
Pfam; PF00083; sugar tr; 1.
PRINTS; PR00171; SUGATKNSPORT.
IIGRAMs; IIGR00879; SP; 1.
PROSITE; PS50850; MFS; 1.
PROSITE; PS00216; SUGAR_IRANSPORT_1; 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; Z99532; CAB16718.1; -. PIR; T43400; T43400.
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                                              Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                   NCBI_TaxID=4896;
                                                                                                                SEQUENCE
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494 AA

STANDARD;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEIFPLHVKGVATGICVLTNWLMAFLVTKEFSSLMEVLRPYGAFWLASAFCIFSVLFTLF 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  527
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              185 VGRFVIGWGVGIASLIIPLYLSEIAPSKIRGRLVIIYVLLITAGQVIAYGIDTAFEHVHN 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     305 LIQEGVRDPFSGSRWQKIVKTFK-ELYFNPSNFRALILACGIQAMQQLSGFNSLMYFSST 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FKLTQGGPGNSSHVAISAPVSAQPVDASVGLAWLAVG--SMCLFIAGFAVGWGPIPWLLM 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DPEETQPLLGPPGGSAPRGRRVFLAAFAAALGPLSFGFALGYSSPAIPSLQRAAPPAPRL
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EXTRACELLULAR (POTENTIAL)
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EXTRACELLULAR (POTENTIAL)
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3B7C5EFF86C596AE CRC64;
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CYTOPLASMIC (POTENTIAL).
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                    transport, Glycoprotein
86 CYTOPLASMIC (PO
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90; Mismatches
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432
575 AA;
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nes 147; Conserv
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GTR3 BOVIN RESULT 11

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                                                                                                                                                                                                                                                                                                                                         Augustin R., Fischer B.; "Glucose transporter expression during bovine preimplantation embryo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- FUNCTION: Facilitative glucose transporter. Probably a neuronal
                                                                                                                                                                          Bos taurus (Bovine).
Makaryota Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinee; Bos.
                          Solute carrier family 2, facilitated glucose transporter, member (Glucose transporter type 3, brain).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     glucose transporter.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- SIMILARITY: Belongs to the sugar transporter family. Glucose transporter subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Augustin R., Navarrete-Santos A., Fischer B.;
"Expression of glucose transporters amongst ruminants.";
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00216; SUGAR_TRANSPORT_1; 1.
PROSITE; PS00217; SUGAR_TRANSPORT_2; 1.
Transmembrane; Sugar transport; Transport; Glycoprotein; Multigene family.

CYTOPLASMIC (POTENTIAL).

TRANSMEM 6 26 1 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases
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7 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
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Interpro; IPR005829; Sug_transporter.
Interpro; IPR003663; Sugar_transpt.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00083; sugar tr; 1.
PRINTS; PR00171; SUGRTRNSPORT.
TIGRFAMS; TIGR00879; SP; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 385-494 FROM N.A.
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SEQUENCE FROM N.A.
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                                                                                                                                                                       Currie M.J., Bassett N.S., Gluckman P.D.,
"Ovine glucose transporter-1 and -3: cDNA partial sequences and
developmental gene expression in the placenta.";
Placenta 18:393-401(1997)
-:- FUNCTION: Facilitative glucose transporter. Probably a neuronal
glucose transporter.
-:- SUBCELLULAR LOCATION: Integral membrane protein.
-:- TISSUB SPECIFICITY: Highly expressed in brain.
-:- SIMILARITY: Belongs to the sugar transporter family. Glucose
  'Isolation of cDNAs and tissue specific expression of ovine glucose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      65 ;
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL)
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InterPro; IPR005826; Sub_transporter.
InterPro; IPR003629; Sug_transporter.
InterPro; IPR003663; Sugar_transpt.
Pfan; PF00083; sugar_tr; 1.
PRINTS; PR00171; SUGRTRNSPORT.
TIGRRAMs; TIGR0879; SP; 1.
PROSITE; PS002650; MFS; 1.
PROSITE; PS00216; SUGAR_TRANSPORT 1; 1.
PROSITE; PS00216; SUGAR_TRANSPORT 2; 1.
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                                  Liamsporters...;
Biochem. Mol. Biol. Int. 37:9-16(1995)
                                                                                                                                                       MEDLINE=97392487; PubMed=9250701;
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                                                                                                  OF 88-248 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                            transporter subfamily
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        282 IFEEAKFKDSSLASVVVGVIQVLFTAVAALIMDRAGRRLLLVLSGVVMVFSTSAFGAYFK 341
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                                                                                                                                                                                                                                                                                                                                                                                                            LGPPGGSAPRGRRVFLAAFAAALGPLSFGFALGY--SSPAI-----PSLORAAPPAPRL 64
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28-FEB-2003 (Rel. 33, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Solute carrier family 2, facilitated glucose transporter, member 3
Glucose transporter type 3, brain).
Ovis aries (Sheep).
Ovis aries (Sheep).
Mammalia; Eutheria; Cetartiodactyla; Nertebrata; Euteleostomi;
Bovidae; Caprinae; Ovis.
                                                                                                                                                                                                                                                                                                                                                            73;
                                                                                                                                                                            N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
                                                                       12 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
DEFINES SUBSTRATE SPECIFICITY (BY
                                                                                                                                                                                                                                                                                                         DB 1; Length 494;
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                                                                                                                                                                                                                                                                                                                                                         96; Mismatches 177; Indels
                                                                                                                                                                                                                               PWFIV -> SLVYC (IN REF. 2)
EC42A3C648CAD23C CRC64;
                             11 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
CYTOPLASMIC (POTENTIAL)
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MEDLINE-96109471; PubMed=8653093;
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                                                                                                                                 357 APVSAQPVDASVGLAWLAVGSMCLFIAGFAVGWGPIPWLLMSEIFPLHVKGVATGICVLT 416
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        -QRAAPPAPRLDDAAASWFGAV
                         LIFAISIATIGSFQFGYNTGVINAPEAIIKDFLNYTLEERSETPPSSVLLTSLWSLSVAI
                                                                                 ACGVASLVAPVYISEIAYPAVRGLLGSCVQLMVVVGILLAYLAGWVL----EWRWLAVLG
                                                                                                                      --CVPPSLMLLLMCFMPETPRFLLTQHRRQE-AMAALRFLWGSEQGWEDPPIGAEQSFH-
                                            VTLGAAAGGVLGGWLVDRAGRKLSLLLCSVPFVAGFAVI---TAAQDVWMLLGGRLLTGL
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Sciurognathi; Muridae; Murinae; Rattus
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MEDLINE=96042339; PubMed=7475896;
Krishnan S. N., Haddad G.G.;
Krishnan S. N., Haddad G.G.;
Life Sci. 56:1193-1197(1995).

-: FUNCTION: Facilitative glucose transporter. Probably a neuronal
                                                                                                                                                                                                                                                                                                                                                                                   007647; Q62729;
01-0CT-1994 (Rel. 30, Created)
01-0CT-1994 (Rel. 30, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
solute carrier family 2, facilitated glucose transporter, member 3
(Glucose transporter type 3, brain).
SLC2A3 OR GLUT3 OR GLUT-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           glucose transporter.
SUBCELLULAR LOCATION: Integral membrane protein.
TISSUE SPECIFICITY: Highly expressed in brain.
SIMILARITY: Belongs to the sugar transporter family. Glucose transporter subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Neuron-specific glucose transporter (NGGT): CNS distribution of GLUT3 rat glucose transporter (RGT3) in rat central neurons.", FEBS Lett. 334:289-295(1993).
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MEDLINE-94063043; PubMed-8243635;
Nagamatsu S., Sawa H., Kamada K., Nakamichi Y., Yoshimoto K.,
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                                                                                                                                                                                                                                                                                                                                                                            493 AA.
        VFLAAFAAALGPLSFGFALGYSSPAIPSL
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EWBL outstation the European Bioinformatics Institute. There are no restrictions on its was by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseeisb-sib.ch). 15; 111 AVITAAQDVWMLLGGRLLTGLACGVASLVAPVYISEIAYPAVRGLLGSCVQLMVVVGILL 171 99 52 GTAKVTPSLVFAVTVATIGSFQFGYNTGVIN-----APETIIKDFLNYTLEERLED AAASWFGAVVTLGA-----AAGGVLG----GWLVDRAGRKLSLLLCSVPFV----AGF Gaps 77; . .) (POTENTIAL) 23.4%; Score 574.5; DB 1; Length 493; 31.1%; Pred. No. 3e-33; EMBL; U19962; BAA03065.1; -.

R EMBL; U1998; AAA62503.1; -.

R InterPro; 1PR00114; MFS.

InterPro; 1PR005828; Sub\_transporter.

InterPro; 1PR005829; Sug\_transporter.

InterPro; 1PR005829; Sug\_transporter.

R InterPro; 1PR0036329; Sugar\_transporter.

R InterPro; 1PR0036329; Sugar\_transporter.

R Pfam; PF00083; Sugar\_tri. 1.

R PROSITE; PS00171; SUGAR\_TRANSPORT.

R PROSITE; PS00216; SUGAR\_TRANSPORT\_2; 1.

R PROSITE; PS00216; SUGAR\_TRANSPORT\_2; 1.

R PROSITE; PS00217; SUGAR\_TRANSPORT\_2; 1.

Transmembrane; Sugar transport; Transport; GPOTENTIAL).

T DOMAIN 1 1 (POTENTIAL).

T DOMAIN 32 64 EXTRACELLULAR (POTENTIAL). 12 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
DEFINES SUBSTRATE SPECIFICITY
SIMILARITY).
N-LINKED (GLCNAC. . .) (POTENT Indels 6 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
7 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
8 (POTENTIAL). EXTRACELLULAR (POTENTIAL) R -> S (IN REF. 2). S -> F (IN REF. 2). H -> Q (IN REF. 2). 745446B59BDF4399 CRC64; GSAPRGRRVFLAAFAALGPLSFGFALGYSSPAIPSLQRAAPPA-3 (POTENTIAL). EXTRACELLULAR (POTENTIAL) EXTRACELLULAR (POTENTIAL) EXTRACELLULAR (POTENTIAL) 2 (POTENTIAL). CYTOPLASMIC (POTENTIAL). 4 (POTENTIAL). CYTOPLASMIC (POTENTIAL). 5 (POTENTIAL). CYTOPLASMIC (POTENTIAL).
9 (POTENTIAL). CYTOPLASMIC (POTENTIAL). 93; Mismatches 176; 10 (POTENTIAL) 11 (POT)

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EMBL;
EMBL;
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                                                                                                                                                                                                 EMBL;
EMBL;
    169 AQVFGLDFILGSEELWPGLLGLTIIPAILQSAALPFCPESPRFLLINRKEEDQATEILQR 228
                                                                                            335
                                                                                                                  337
                                                                                                                                                              387
                                                                                                                                                                                      455
                                                                                                                                                                                                          446
                                                                                                                                                    229 LWGTPDVIQEIQEMKDESIRMSQEKQVTVLELFKSPSYFQPLLISVVLQLSQQFSGINAV
                                                                                                                                                                                                 MEDILINE=98138446; PubMed=9477959; Seatter M.J., dela Rue S.A., Porter L.M., Gould G.W.; Seatter M.J., de la Rue S.A., Porter L.M., Gould G.W.; "QLS motif in transmembrane helix VII of the glucose transporter family interacts with the C.1 (position) of D-glucose and is involved in substrate selection at the exofacial binding site.";
AYLAG--WVL--EWRWLAVLG--CVPPSLMLLLMCFMPETPRFLLTQHRRQ-EAMAALRF
                                              LWGSE-----QGWEDPPIGAEQSFH---LALLRQPGIYKPFIIGVSLMAFQQLSGVNAV
                                                                                          276 MFYAETIFEEAKFKDSSLASVVVGVIQVLFTAVAALIMDRAGRRLLLVLSGVVMVFSTSA
                                                                                                         289 FYYSTGIFQDAGVQEPIYATIGAGVVNTIFTVVSLFLVERAGRRTLHMI------
                                                                                                                                      336 FGAYFKLTQGGPGNSSHVAISAPVSAQPVDASVGLAWLAVGSMCLFIAGFAVGWGPIPWL
                                                                                                                                                                                   LMSEIFPLHVKGVATGICVLTNWLMAFLVTKEFSSLMEVLRPYGAFWLASAFCIFSVLFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. Stuart C.A., Wen M., Wood T.G., Stuart C.A., Wen K.G., Acosta M., Wood T.G., "Resistance and expression of glucose transporters in human skeletal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=89008414; PubMed=3170580;
Kayano T., Fukumoto H., Eddy R.L., Fan Y.-S., Byers M.G., Shows T.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUB-Articular cartilage;
Neama G., Richardson S., Bell S., Carter S., Mobasheri A.;
"Molecular characterization and cloning of glucose transporters in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bell G.I.;
"Evidence for a family of human glucose transporter-like proteins.
Sequence and gene localization of a protein expressed in fetal
skeletal muscle and other tissues.";
J. Biol. Chem. 263:15245-15248 (1988).
                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                           GTR3_HUMAN STANDARD; PRT; 496 AA.
191169; QGUG15;
01-JUL-1989 (Rel. 11, Created)
01-JUL-1989 (Rel. 11, Last sequence update)
501-JUL-1989 (Rel. 11, Last annotation update)
Solute carrier family 2, brain)
(Glucose transporter type 3, brain).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUBEFeral brain;
Blum H., Bauersachs S., Mewes H.-W., Gassenhuber J., Wiemann S.;
Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                   447 SFKVPETKGRTFEDITRAFEGO 468
                                                                                                                                                                                                                              LECVPETKGKTLEQITAHFEGR 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      human articular chondrocytes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 302-453 FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBSTRATE SPECIFICITY SITE.
                                                                                                                                                                                                                                                                                                                                                                                                       sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                         SLC2A3 OR GLUTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   muscle.";
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Biochemistry 37:1322-1326(1998).
-!- FUNCTION: Facilitative glucose transporter. Probably a neuronal
                                   glucose transporter.
SUBCELLULAR LOCATION: Integral membrane protein.
TISSUE SPECIFICITY: Highly expressed in brain.
SIMILARITY: Belongs to the sugar transporter family. Glucose transporter subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (POTENTIAL)
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DEFINES SUBSTRATE SPECIFICITY (BY
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PROSITE; PS00216; SUGAR_TRANSPORT_1; 1.
PROSITE; PS00217; SUGAR_TRANSPORT_2; 1.
Transmembrane; Sugar transport; Transport; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
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EXTRACELLULAR (POTENTIAL)
2 (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
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EXTRACELLULAR (POTENTIAL)
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EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
7 (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                             GK; P11169; -. MIM; 138170; -. GO; 0005555; F:glucose transporter activity; TAS. GO; GO:0015758; P:glucose transport; TAS. InterPro; IPR007114; MFS.
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E -> Q (IN REF. 3).
G -> S (IN REF. 3).
VV -> LL (IN REF. 3).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR005828; Sub_transporter.
InterPro; IPR005829; Sug_transporter.
InterPro; IPR003663; Sugar_transpt.
Pfam; PP00083; Sugar_tr; 1.
                                                                                                                                                                                                                                                                                          AF274892; AAF82116.1; AF274889; AAF82116.1; JOINED. AF274891; AF274891; JOINED. AF82116.1; JOINED. AF1274891; AAF82116.1; JOINED. AAV34634; AAK56796.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PR00171; SUGRTRNSPORT.
TIGREAMS; TIGR00879; SP; 1.
                                                                                                                                                                                                                                                                              EMBL; M20681; AAB61083.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Genew; HGNC:11007; SLC2A3.
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310
321
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PIR; T14798; T14798.
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DOMAIN
TRANSMEM 6
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                                                                                                                                                     133 ACGVASLVAPVYISEIAYPAVRGLLGSCVQLMVVVGILLAYLAG--WVL--EWRWLAVLG 188
                                                                                                                                                                                           -----LALLRQPGIYKPFIIGVSLMAFQQLSGVNAVMFYAETIFEEAKFKDSSLASV 296
                                                                                                                                                                                                                                                                    250 SQEKQVTVLELFRVSSYRQPIIISIVLQLSQQLSGINAVFYYSTGIFKDAGVQEPIYATI 309
                                                                                                                                                                                                                                                                                              297 VVGVIQVLFTAVAALIMDRAGRRLLLVLSGVVMVFSTSAFGAYFKLTQGGPGNSSHVAIS 356
                                                                                                                                                                                                                                                                                                          APVSAQPVDASVGLAWLAVGSMCLFIAGFAVGWGPIPWLLMSEIFPLHVKGVATGICVLT 416
                                                                                                                                                                                                                                                                                                                                              NWLMAFLVTKEFSSLMEVLRPYGAFWLASAFCIFSVLFTLFCVPETKGKTLEQITAHFEG 476
                                                                                                                                                                                                                                                                                                                                                                                   --CVPPSLMLLLMCFMPETPRFLLTQHRRQE-AMAALRFLWGSEQGWEDPPIGAEQSFH- 244
                                                                                                        75
                                                                                                                           69
                                                                                                      26 VFLAAFAALGPLSFGFALGYSSPAIPSLQR------AAPPAAPRLDDAAASWFGAV
                                                                                                                         10 LIFAITVATIGSFOFGYNTGVINAPEKIIKEFINKTLTDKGNAPPSEVLLTSLWSLSVAI
                                                                                                                                          76 VTLGAAAGGVLGGWLVDRAGRKLSLLLCSVPFVAG----FAVITAAQDVWMLLGGRLLTGL
                                                                                                                                                                                                                                      190 FTILPAILQSAALPFCPESPRFLLINRKBEENAKQILQRLWGTQDVSQDIQEMKDESARM
                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-UUL-1993 (Rel. 26, Created)
01-UUL-1993 (Rel. 26, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Solute carrier family 2, facilitated glucose transporter, member 3 Glucose transporter type 3, brain).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Glucose transporter expression in brain. CDNA sequence of mouse GLUT3, the brain facilitative glucose transporter isoform, and identification of sites of expression by in situ hybridization."; 0, Blol. Chem. 267:467-472(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nagamatsu S., Kornhauser J.M., Seino S., Mayo K.E., Steiner D.F.
                                                                                      51;
                                                                  DB 1; Length 496;
                                                                  23.2%; Score 570.5; DB 1; Length 31.6%; Pred. No. 5.8e-33; ive 88; Mismatches 190; Indels
DN -> NH (IN REF. 3).
F -> C (IN REF. 3).
H -> Y (IN REF. 3).
F -> L (IN REF. 3).
E -> G (IN REF. 3).
K -> G (IN REF. 3).
W, F601CD6892F16516 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               493 AA
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                                                53924 MW;
                                                                                    152; Conservative
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358
376
425
432
482
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                                               496 AA;
                                                                           Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10090;
 357
376
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P32037;
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CONFLICT
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Best Local
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                                                                                                                                                                   Attaubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haich F.
A platchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleron M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Torshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Robark S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunnarane P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield V.S. N., Krzywinski M.I., Skalska U., Smailus D.E.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
Fromeration and initial analysis of more than 15,000 full-length
Proc. Natl. Acad. Sci. U.S.A. 9916899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Takeda J., Minokoshi Y., Yasuda K., Kayano T., Graeme B.I., Submitted (JUL-1994) to the EMBL/GenBank/DDBJ databases.
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EXTRACELLULAR (POTENTIAL)
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PROSITE; PS00217; SUGAR TRANSPORT 2; 1.
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InterPro; IPR003663; Sugar_transpt.
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MEDLINE=22388257; PubMed=12477932;
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PRINTS; PR00171; SUGRIRNSPORT.
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InterPro; IPR005828; Sub
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                                                                                         SEQUENCE FROM N.A.
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2 (POTENTIAL)

CYTOPLASMIC (POTENTIAL).  3 (POTENTIAL).  EXTRACELLULAR (POTENTIAL).  5 (POTENTIAL).  5 (POTENTIAL).  6 (POTENTIAL).  6 (POTENTIAL).  6 (POTENTIAL).  7 (POTENTIAL).  8 (POTENTIAL).  9 (POTENTIAL).  9 (POTENTIAL).  10 (POTENTIAL).  11 (POTENTIAL).  12 (POTENTIAL).  13 (POTENTIAL).  14 (POTENTIAL).  15 (POTENTIAL).  16 (POTENTIAL).  17 (POTENTIAL).  18 (POTENTIAL).  19 (POTENTIAL).  10 (POTENTIAL).  11 (POTENTIAL).  12 (POTENTIAL).  13 (POTENTIAL).  14 (POTENTIAL).  15 (POTENTIAL).  16 (POTENTIAL).  17 (POTENTIAL).  18 (POTENTIAL).  19 (POTENTIAL).  10 (POTENTIAL).  11 (POTENTIAL).  12 (POTENTIAL).  13 (POTENTIAL).  14 (POTENTIAL).  15 (POTENTIAL).  16 (POTENTIAL).  17 (POTENTIAL).  18 (POTENTIAL).  19 (POTENTIAL).  10 (POTENTIAL).  10 (POTENTIAL).  11 (POTENTIAL).  12 (POTENTIAL).  13 (POTENTIAL).  14 (POTENTIAL).  15 (POTENTIAL).  16 (POTENTIAL).  17 (POTENTIAL).  18 (POTENTIAL).  18 (POTENTIAL).  19 (POTENTIAL).  10 (POTENTIAL).  10 (POTENTIAL).  11 (POTENTIAL).  12 (POTENTIAL).  13 (POTENTIAL).  14 (POTENTIAL).  15 (POTENTIAL).  16 (POTENTIAL).  17 (POTENTIAL).  18 (POTENTIAL).  19 (POTENTIAL).  10 (POTENTIAL).  10 (POTENTIAL).  11 (POTENTIAL).  12 (POTENTIAL).  13 (POTENTIAL).  14 (POTENTIAL).  15 (POTENTIAL).  16 (POTENTIAL).  17 (POTENTIAL).  18 (POTENTIAL).  19 (POTENTIAL).  10 (POTENTIAL).  10 (POTENTIAL).  11 (POTENTIAL).  12 (POTENTIAL).  13 (POTENTIAL).  14 (POTENTIAL).  15 (POTENTIAL).  16 (POTENTIAL).  17 (POTENTIAL).  18 (POTENTIAL).  19 (POTENTIAL).  10 (POTENTIAL).  10 (POTENTIAL).  11 (POTENTIAL).  11 (POTENTIAL).  12 (POTENTIAL).  13 (POTENTIAL).  14 (POTENTIAL).  15 (POTENTIAL).  16 (POTENTIAL).  17 (POTENTIAL).  18 (POTENTIAL).  19 (POTENTIAL).  10 (POTENTIAL).  10 (POTENTIAL).  11 (POTENTIAL	23.2%; Score 569.5; DB 1; Length 493; ; Conservative 86; Mismatches 176; Indels 73; Gaps 13; AAFAAALGPLSFGFALGYSSPAIPSLQRAAPPAPRLDDAAA 69	AVTVATIGSFQFGYNTGVINAPETILKDFLNYTLEERLEDLPSEGLLTALW 63 SWFGAVVTLGAAAGGVLGGWLVDRAGRKLSLLLCSVPFVAGFAVITAAQDVWML1 124		WEDPPIGAEQSFHLALLRQPGIYXPFIIGVSLMAFQQLSGVNAVMFYAETIFEBAKF 288	AGRRTLH GSMCLFI. :: ::: VAILIYV	ATGICVLTNWLMAFLVTKEFSSLMEVLRPYGAFWLASAFCIFSVLFTLFCVPETKGKTLE 468
1119 11144 11144 111444 111444 111444 1114 11144 11144 11144 11144 11144 11144 11144 11144 11144 11144 114	23. 31. vative LSFGFA	FQFGYN GAAAGC GGMIGS	CGVASI   :: CGLCTC -CVPPE :  IIIPAI	QSFH QEKQVT VGVIQV	AĞVVNI PVSAQE :  TISLLI	WLMAFI 
86 946 1115 1125 1125 1154 1154 1154 1155 1156 1156 1156 115	Similarity 4; Conserva AAFAAALGPLS	AVTVATIGSFQFGYNTGVIN- SWFGAVVTLGAAAGGVLGGWL   ::    SLCVAIFSVGGMIGSFSVGLF	GGRLLTGLA           LGRLLIGIF WRWLAVLG-   :     ELWPGLLGL	WEDPPIGAEQSFH-	QEPIYATIG NSSHVAISA : :: GMAVCSVFW	ATGICVLTN   :     AIAVAGCCN QITAHFEGR             DIARAFEGQ
DOMAIN TRANSMEM DOMAIN TRANSME	Query Match Best Local S: Matches 154	13 70 64	125 122 181 182	232 242 289	302 349 341	4 4 4 4 4 4 4 6 9 4 6 0 9 4 6 9 9 4 6 9 9 9 9 9 9 9 9 9 9 9 9 9
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Search completed: September 27, 2004, 19:27:12 Job time : 28 secs

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RESULT 1
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-MODEL=frame+_D2n.model -DEV=xlp
-Q=/Cqn2_1/USPFTO spool_p/USP0886594/runat_27092004_170631_13388/app_guery.fasta_1.647
-Q=/Cqn2_1/USPFTO spool_p/USP0886594/runat_27092004_170631_13388/app_guery.fasta_1.647
-DB=GenEmbl -QFMT=fastap -SUFFIX=rge -MINMATCH=0.1_-LOOPCI=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=bitsen.m62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXIR=200000000
-USER=US09886954 @CGN 1 1.5600 @runat_27092004_170631_13388 -NCFU=6 -ICFU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DBV TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XAAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
                                                                                                                                                                                                                                         September 28, 2004, 00:53:58; Search time 4589 Seconds (without alignments) 4505.258 Million cell updates/sec
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1 MTPEDPEETQPLLGPPGGSA......CVPETKGKTLEQITAHFEGR 477
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Ygapop 10.0 , Ygapext
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Maximum DB seq length: 2000000000
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31: em_htg_hum:*
31: em_htg_other:*
32: em_htg_other:*
33: em_htg_pun:*
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35: em_htg_pun:*
36: em_htg_vat:*
37: em_htg_vat:*
38: em_sy:*
49: em_htgo_hum:*
41: em_htgo_hum:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Score         Match Length DB         ID         Description           2457         100.0         2080         6 AX17974         AX179740         Sequence           2457         100.0         2080         6 AX17974         AX076657         AX076657         AX076657         AX076657         AX076657         AX076657         AX076657         AX076659         AX076667         AX076669         AX076669         AX076667         AX076669         AX076667         AX076669         AX076667         AX076669         AX076667         AX076669         AX076699         AX			₩			SUMMARIES	
1         2457         100.0         2165         9         RCA179740         AXX179740         AXX179740         SEQUENCE           2         2448         99.6         2147         9         RSA245937         AXX77667         SEQUENCE           2         2448         99.6         2217         6         AX076669         AX077667         SEQUENCE           2         2448         99.6         2217         6         AX076669         AX077667         SEQUENCE           2         2448         99.6         1287         10         NMU1785935         AX077667         SEQUENCE           2         2159         81.0         10         NMU1785936         AX077667         SEQUENCE           1         2156         87.7         1843         10         AX077667         AX077667         SEQUENCE           1         2156         87.9         10         AX0776693         AX077667         SEQUENCE           1         2150         87.2         10         AX077679         AX077679         AX077679         AX077679           1         2150         87.2         10         AX077679         AX077679         AX077679         AX077679         AX077679	Result No.	COL	Query Match	Length	Ω		escripti
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AX179740 AX179740 AX179740 DEPUNITION Sequence 28 from Patent WO0146258. ACCESSION AX179740 VBRSION AX179740. VBRSION AX179740.1 GI:15132104 KEYWORDS . SOURCE Homo sapiens (human)	NISM NCE ORS	TITLE Transporters and ion channels JOURNAL Patent: WO 0146258-A 28 28-JUN-2001; JOURNAL Incyte Genomics, Inc. (US) FEATURES 1. 2080   /organism="Homo sapiens" / nol Type="unassigned DNR"	cores:	Pred. No.:       2.44e-167       Length:       2080         Score:       2457.00       Matches:       477         Percent Similarity:       100.00\$       Conservative:       0         Best Local Similarity:       100.00\$       Mismatches:       0         Query Match:       100.00\$       Indels:       0         DB:       6       Gaps:       0	4A-1       (1-477)       x AX179740       (1-2080)         1       MetThrProGluAspProGluGluThrGlnProLeuLeuGlyProProGlyGlySerAla       2         1	21 ProArgGlyArgArgValPheLeuAlaAlaPheAlaAlaAlaLeuGlyProLeu 	ProPro 6	Qy 61 AlaProArgLeuAspAspAlaAlaAserTrpPheGlyAlaValValThrLeuGlyAla 80	SerLeu 10        AGCCTC 34			141 AlaProValTyrIleSerGluIleAlaTyrProAlaValArgGlyLeuLeuGlySerCys 	Qy 161 ValGinLeuMetValValOlytleLeuLeuAlaTyrLeuAlaGlyTrpValLeuGlu 180	Qy 181 TrpArgTrpLeuAlaValLeuGlyCysValProProSerLeuMetLeuLeuLeuMetCys 200

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Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Banaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Ugdin, F.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellaro, N.A., Peters, G.J., Abramson, R.D., Mullek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.M., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S., Sanchez, A., Whilring, M., Madan, A., Rodrigues, S., Sanchez, A., Whilring, M., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E., Schnerch, A., Schein, J.E., Onnes, S.J. and Marra, M.A. Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 30 Row: n Column: 3
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 21361448.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: nisc_mgo@nhgri.nih.gov
Akhter.N., Ayele.K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Blakesley,R.W., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
Maduro,Q.L., Mastello,C., Maskeri,B., Mastrian,S.D.,McCloskey,J.C.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Young,A., Zhang,L.-H. and Green,E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
Submitted (07-DE-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /codon_start=1
/product="solute carrier family 2, (facilitated glucose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NIH-MGC Project URL: http://mgc.nci.nih.gov
On Dec 19, 2003 this sequence version replaced gi:17512129.
Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
2 (bases 1 to 2145)
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db_xref="LocusID:29988"
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Web site: http://www.nisc.nih.gov/
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'gene="SLC2A8"
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AUTHORS
TITLE
JOURNAL
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COMMENT

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SVLFTLFCVPETKGKTLEQITAHFEGR"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 TrpMetLeuLeuGlyGlyArgLeuLeuThrGlyLeuAlaCysGlyValAlaSerLeuVal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       46 ATGACGCCCGAGGACCCAGAGGAAACCCAGCCGCTTCTGGGGCCTCCTGGCGGCAGCGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ProArgGlyArgArgValPheLeuAlaAlaPheAlaAlaAlaLeuGlyProLeuSerPhe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 226 GCCCCGCGCCTGGACGACGCCGCCTCCTGGTTCGGGGCTGTCGTGACCCTGGGTGCC
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Best Local Similarity: ,
Query Match:
DB:
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SVLFTLFCVPEIKGKTLEQITAHFEGR"
                                                                                                                                                                                                                                                                                                                                                                            Lausanne,
  Pharmacology
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Submitted (02-SEP-1999) Ibberson M.R., Institute of Pharma and Toxicology, University of Lausanne, Rue du Bugnon 27,
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Matches:
Conservative:
Mismatches:
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                                                                                              source
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      JOURNAL
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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GLUTXI, a novel mammalian glucose transporter expressed in the central nervous system and insulin-sensitive tissues
J. Biol. Chem. 275 (7), 4607-4612 (2000)
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  AlaLeuArgPheLeuTrpGlySerGluGlnGlyTrpGluAspProProIleGlyAlaGlu
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and Uldry, M

Ibberson, M.

Glutx polypeptide family and nucleic Patent: WO 0104145-A 118-JAN-2001; University of Lausanne (CH) Location/Qualifiers

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SVLFTLFCVPEIKGKTLEQITAHFEGR"
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DNA

AX076667 2217 bp Sequence 1 from Patent W00104145. AX076667

GI:12711198

AX076667.1

DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM

AX076667 LOCUS Homo sapiens (human) Homo sapiens

Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

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Direct Submission
Submitted (16-JUJ-1998) H. Joost, Institute of Pharmacology and Toxicology, Technical University Aachen, Wendlingweg 2, D-52057 Aachen, FRG
facilitator family
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                  CAGAGCTITCACCTGGCCTGCTGCGGCAGCCCGGCATCTACAAGCCCTTCATCATCATCGCC
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                                                                                  PheMetProGluThrProArgPheLeuLeuThrGlnHisArgArgGlnGluAlaMetAla
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo
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Mammalia; Butheria; Rodentia;
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                                                                                                                                                                                                                                                                                                            Submitted (02-SEP-1999) Ibberson M.R., Institute of Pharmacology and Toxicology, University of Lausanne, Rue du Bugnon 27, Lausanne, CH-1005, SWITZERLAND
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                                                                                                   Vertebrata; Euteleostomi;
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                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleosto
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
 gene)
                                                                                                                                                         Ibberson, M., Uldry, M. and Thorens, B.
GLUTX1, a novel mammalian glucose transporter expressed in central nervous system and insulin-sensitive tissues
J. Biol. Chem. 275 (7), 4607-4612 (2000)
10671487
   for glucose transporter (GLUTX1
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Mismatches:
Indels:
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/mol_type="mRNA"
/db_xref="taxon:10116"
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nsporter; GLUTX1
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AJ245935.1 GI:7018604
glucose transporter; GLUTX1
Rattus norvegicus (Norway rr
Rattus norvegicus
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 norvegicus mRNA
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                                AlaProValTyrIleSerGluIleAlaTyrProAlaValArgGlyLeuLeuGlySerCys
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AlaPheTrpLeuAlaSerAlaPheCysIlePheSerValLeuPheThrLeuPheCysVal
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/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/tissue type="testis"
1. .1490
                                                                                                                                                                 glucose transporter 8; GLUT8 gene.
Mus musculus (house mouse)
Mus musculus
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                                                        TGGATGCTGCTCGGAGGCCGCTCCTCACCGGCCTAGCCTGCGGAGTCGCCTCATTAGTG 449
                                                                                                                                                    AlaProValTyrIleSerGluIleAlaTyrProAlaValArgGlyLeuLeuGlySerCys 160
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                                                                                                                                                                                                                                                                                                                                                AlaLeuArgPheLeuTrpGlySerGluGlnGlyTrpGluAspProProIleGlyAlaGlu 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          GluThrilePheGluGluAlaLysPheLyaAspSerSerLeuAlaSerValValValGly 299
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                                                                                                                                                                    GCACCGGTCTATATCTCGGGAAATCGCCTACCCAGCCGTTCGAGGGACTGCTCGGCTCCTGT 509
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                       GCGGCAGGGGCGTGCTGGGGCTGGCTCCTGGACCGTGCAGGCGCAAGCTGAGCCTC
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                                                   MMU17802 1490 bp mRNA linear ROD 13-MAY-2000
Mus musculus mRNA for glucose transporter 8 (GLUT8 gene).
459
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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J. Biol. Chem. 275 (21), 16275-16280 (2000)
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Submitted (16-JUL-1998) H. Joost, Institute of Pharmacology and
Toxicology, Technical University Aachen, Wendlingweg 2, D-52057
Aachen, FRG
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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419

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mRNA linear ROD 23-JUN-2000
GLUT8 mRNA, complete cds.
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1483. 1843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Carayannopoulos, M.O., Chi, M.M., Cui, Y., Pingsterhaus, J.M., McKnight, R.A., Mueckler, M., Devaskar, S.U. and Moley, K.H. GLUT8 is a glucose transporter responsible for insulin-stimulated
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 1843)
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      CICTICATECTGCTGCCTTTGCGGTGGGCTGGGGACCCATCCCCTGGCTCCTCATGTCAGAG
                                                                  IlePheProLeuHisValLysGlyValAlaThrGlyIleCysValLeuThrAsnTrpLeu
                                                                                              ATCTTCCCTCTGCATGTCAAGGGTGTGGCTACCGGCATCTGTGTCTCTCCCAACTGGTTC
                                                                                                                                                                             MetAlaPheLeuValThrLysGluPheSerSerLeuMetGluValLeuArgProTyrGly
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Proc. Natl. Acad. Sci. U.S.A. 97 (13), 7313-7318 (2000)
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Moley, K.H., Carayannopoulos, M.O. an
Direct Submission
Submitted (07-FEB-2000) OB/Gyn, Was
Ave, St. Louis, MO 63110, USA
Location/Qualifiers
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Mus musculus glucose transporter
AF232061 GI:8671757
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Pred. No.:
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KEYWORDS
SOURCE
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                       CCCGCGGGGCCGCCGGGTCTTCCTCGCTTCGCCGCCGCTCTGGGACCCCTCAGCTTC
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Chordata, Craniata, Vertebrata, Euteleostomi, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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Submitted (02-SEP-1999) Ibberson M.R., Institute of Pharmacology
and Toxicology, University of Lausanne, Rue du Bugnon 27, Lausan
CH-1005, SWITZERLAND
                                                                                 400 IlePheProLeuHisValLySGlyValAlaThrGlyIleCySValLeuThrAsnTrpLeu
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                             1218 ATCTTCCCTCTGCAIGTCAAGGGTGTGGCTACCGGCATCTGTGTCCTCACCAACTGGTTC
                                                                                                                                                                                             SerAlaGlnProValAspAlaSerValGlyLeuAlaTrpLeuAlaValGlySerMetCys
                                                                    LeuPhelleAlaGlyPheAlaValGlyTrpGlyProIleProTrpLeuLeuMetSerGlu
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GLUTX1, a novel mammalian glucose transporter express
central nervous system and insulin-sensitive tissues
20138191
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protein id="CAB75719.1"
db_xref="G1:7018607"
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/db_xref="taxon:10090"
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1. .2072
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Mus musculus (house mouse)
Mus musculus
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/gene="GLUTX1"
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Mammalia; Eutheria;
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Glucose transporter 8.
Rattus norvegicus (Norway rat.)
Rattus norvegicus (Sorway rat.)
Rattus norvegicus; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae;
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Submitted (08-OCT-1999) Kenichi Ishibashi, Jichi Medical School,
Pharmacology; Minami-kawachi, Kawachi, Tochigi 329-0498, Japan
(E-mail:Kishiba@jichi.ac.jp, Tel:81-285-58-7326,
                                                                              PhelysleuThrGlnGlyGlyProGlyAsnSerSerHisValAlalleSerAlaProVal
IlePheProLeuHisValLysGlyValAlaThrGlyIleCysValLeuThrAsnTrpLeu
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Ishibashi,K.
Molecular cloning of a new putative glucose ipublished Only in DataBase (2000)
Ishibashi,K.
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109. .1548
/gene="glut8"
/note="Glut8 has 12 transmembrane
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/protein_id="BAA94383.1"
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/organism="Rattus norvegicus"
/db_xref="Raxon:10116"
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Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                       GlullePheProLeuHisValLySGlyValAlaThrGlyIleCysValLeuThrAsnTrp
                                             AlaGluThrIlePheGluGluAlaLysPheLysAspSerSerLeuAlaSerValValVal
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Kato,S. and Kimura,T.
Human proteins having hydrophobic domains
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/b_xref="G1:1458216"
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CVAPSFMLLLMCFMPETPRFLLSQHKHQEAMAAMQFLWGYAQGWEEPPIGAQHQDFHV
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1 (bases I to 1012)
Augustin,R., Navarrete-Santos,A. and Fischer,B.

Direct Submission
Submitted (13-NOV-2000) Anatomy and Cell Biology, Faculty of Submitted, Martin Luther University Halle, Grosse Steinstrasse.
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/organism="Bos taurus"
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MAFLVTKEFSSLMFVLRPYGAFWLASAFCIFGVLFTIACVPETKGKTLEQITAHFEGR
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Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,
Susanna Chan, Readman Chiu, Chris Fjell, Brin Garland, Ran Guin,
Letticia Heiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo
Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven
Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline
Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott,
Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy,
George Yang, Scott Zuyderduyn, Marco Marra.
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Danio rerio cDNA clone MGC:56364 IMAGE:5604396, complete cds.
BC049409
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Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Sumio Sugano
CDNA Library Preparation: Dr. Sumio Sugano
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Genome Sequence Centre,
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DALSSAGTFWMFSALCASNVVFTAFFVPETKGKTLEEIQAGFKGTRMR"
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| AIGITCTAIGIGGCAGAGIGCTCACIGGTITGGCCAGIGGAGTGACCTCTCTAGITGIA 601
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Clone distribution: MGC clone distribution information can be for through the I.M.A.G.B. Consortium/LLNUs at: http://image.llnl.gov Series: IRAK Plate: 1.O4 Row: b Column: 18
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, Similarity but not identity to protein.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            257. .1624
Anote="sugar tr; Region: Sugar (and other) transporter"
/db_xref="CDD:pfam00083"
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protein id="AAH9409.1"
db_xref="GI:29436434"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1929
282
63
122
19
                                                                                                                                                                                                   male"
                                                                                                                            /organism="Danio rerio"
/mol type="mRNA"
/db_xref="taxon:7955"
/clone="MGC:56364 IWAGE:5604396"
/tissue type="Whole body, adult male"
/lab host="DH108"
/note="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches:
Conservative:
Mismatches:
Indels:
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58.02%
57.45%
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Best Local Similarity:
Query Match:
DB:
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Search completed: September 28, 2004, 03:28:36 Job time: 4617 secs

358, App 1685, Ap 1685, Ap 109, App 132422,

Sequence Sequence Sequence Sequence

Sequence Sequence

701.5 682

666.5 639 620.5 609.5

Sequence

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2067.5 11554.5 1268.9 958.5 958.5 958.5 958.5

26596, A 249661, A 26561, A 357, App 820, App 440591, A 223421, A 22342, A

Sequence Seq

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| US-10-116-851-28 |
| US-10-116-851-28 |
| US-10-16-95-29 |
| US-10-15-95-29 |
| US-10-15-96-109 |
| US-10-172-118-1685 |
| US-10-184-187 |
| US-10-282-122A-40124 |
| US-09-938-842A-1769 |
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2457
1 MTPEDPBETQPLLGPPGGSA.......CVPETKGKTLEQITAHFEGR 477
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                   - nucleic search, using frame_plus_p2n model
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Maximum Match 100%
Listing first 45 summaries
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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Maximum DB seq length: 200000000
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Sequence 507, App Sequence 1341, Ap Sequence 1341, Ap Sequence 248, App

US-10-342-887-1341 US-10-172-118-1341 US-10-170-385-248

574.5 571 570.5 570.5 570.5

Sequence 79, Appl Sequence 35021, A Sequence 1769, Ap Sequence 96711, A

Sequence 6734, Ap Sequence 47239, A Sequence 1627, Ap Sequence 1627, Ap Sequence 2331, Ap Sequence 2331, Ap Sequence 3312, Ap Sequence 3132, Ap Sequence 40124, Ap

Sequence Sequence Sequence

1386 2045 2045 2051 2190 1419 1395 1767 1395 13395 13395 1473

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604.5 604.5 604.5 603 598.5

6674772

Sequence 1769, Ap Sequence 1769, Ap

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SUBJECTANT: INFORMATION:

APPLICANT: Tang, Y. Tom
APPLICANT: Tang, Y. Tom
APPLICANT: Abundi, Vinod
APPLICANT: Abundi, Vinod
APPLICANT: Abundi, Vinod
APPLICANT: Abundi, Vinod
APPLICANT: Ren, Feiyan
APPLICANT: Ren, Feiyan
APPLICANT: Pranac, Radoje T.
ITIEB OF INVENTION: No. US20030219743A1e1 Nucleic Acids and
ITIEB OF INVENTION: No. US20030219743A1e1 Nucleic Acids and
ITIEB OF INVENTION: POLYPEPTIOSE
FILE REFERENCE: 79COL-04-02
FILE REFERENCE: 79COL-04-02
FRIOR FILING DATE: 2000-09-22
FRIOR APPLICATION NUMBER: 09/667,298
FRIOR FILING DATE: 2000-05-18
FRIOR FILING DATE: 2000-05-18
SRIOR APPLICANT: Abundian Struck
SEQ ID NOS: 178
SEQ ID NO 137
INNERS DE L'agenes Version 2.0
Sequence 137, Application US/10115831 Publication No. US20030219743A1 GENERAL INFORMATION:
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28 09:09:40 2004

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TITLE OF INVENTION: TRANSPORTERS AND ION CHANNELS
FILE REFERENCE: PI-0005 PCT
CURRENT APPLICATION NUMBER: US/10/168,651
PRIOR APPLICATION NUMBER: 60/172,000; 60/176,083; 60/177,332; 60/178,572; 60/179,758
60/181,625
PRIOR PILING DATE: 1999-12-23; 2000-01-14; 2000-01-21; 2000-01-28; 2000-02-02;
2000-02-10
NUMBER OF SEQ ID NOS: 54
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Sequence 28, Application US/10168651
Publication No. US20030171275A1
GENERAL INPORMATION:
APPLICANT: INCYTE GRNOWICS, INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BAUGHN, Mariah R.
BUREORD, Neil
AU-YOUNG, Janice
LU, Dyung Aina M.
YANG, Junming
REDDY, Roopa
LAL, Preeti
HILLMAN, Jennifer L.
AZIRZAL, Yalda
YUE, Henry
NGUYEN, Danniel B.
YAO, Monique G.
GANDHI, Ameeni R.
TANG, Y. Tom
KHANG, Y. Tom
KHANG, PETTANA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 54
SOFTWARE: PERL Program
SEQ ID NO 28
LENGTH: 2080
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APPLICANT:
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                                                                                                         Percent Similarity:
Best Local Similarity:
Query Match:
DB:
TYPE: DNA
ORGANISM: Homo
                     FEATURE:
NAME/KEY: CDS
LOCATION: (4).
                                            ; LOCATION: (4)
US-10-115-831-137
                                                                              Alignment Scores: Pred. No.:
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                               ACCATCTTTGAAGAGGCCAAGTTCAAGGACAGCAGCCTGGCCTCGGTCGTCGTGGTCT
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        ThrilePheGluGluAlaLysPheLysAspSerSerLeuAlaSerValValGlyVal
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| Publication No. US20030219743A1
| GENERAL INFORMATION:
| APPLICANT: Tang, Y. Tom
| APPLICANT: Liu, Chenghua
| APPLICANT: Liu, Chenghua
| APPLICANT: Rannac, Radoje T.
| TITLE OF INVENTION: No. US20030219743A1e1 Nuc;
| TITLE OF INVENTION: Polypeptides
| FILE REFERENCE: 792C1P2ADIV
| CURRENT APPLICATION NUMBER: 09/67, 298
| PRIOR FILING DATE: 2000-09-22
| PRIOR FILING DATE: 2000-05-18
| NUMBER OF SEQ ID NOS: 178
| SOFTWANKE: PL FIL Genes Version 2.0
| SEQ ID NO 138
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                                                           ; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030171275A1 1416107CB1
US-10-168-651-28
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Matches:
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Mismatches:
Indels:
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                                                                                                                                                                    3.51e-254
2457.00
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100.00%
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                         Percent Similarity:
Best Local Similarity:
Query Match:
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Percent Similarity: 85.53\$ Conservative: 0 Best Local Similarity: 85.53\$ Mismatches: 0 Query Match: 84.15\$ Indels: 69 DB: 1 US-09-886-954A-1 (1-477) x US-10-115-831-138 (1-1655)	Qy 1 MetThrProGludspProGluGluThrGlnProLeuLeuGlyProProGlyGlySerAla 20	aAlaLeuGly          rGCCCTGGG	ProdlalleProSerLeuGlnArgAlaAl		81 AlaAlaGlyGlyValLeuGlyGlyTrpLeuValAspArgAlaGlyArgLysLeuSerLeu	Db 222 222 Oy 101 LeuLeuCysSerValProPheValAlaGlyPheAlaValIleThrAlaAlaGlnAspVal 120	Db 222 222	Qy 121 TrpMetLeuLeuGlyGlyArgLeuLeuThrGlyLeuAlaCysGlyValAlaSerLeuVal 140	141 AlaProValTyrileSerGluIl		Qy 161 ValGlnLeuMetValValValGlyIleLeuLeuAlaTyrLeuAlaGlyTrpValLeuGlu 180	TPLeualaValLeuGlyCysValProProSerLeuMetLeuLeuLeuMet Cys	QY 201 PheMetProGluThrProArgPheLeuLeuThrGlnHisArgArgGlnGluAlaMetAla 220	Qy 221 AlaLeuArgPheLeuTrpGlySerGluGlnGlyTrpGluAspProProlleGlyAlaGlu 240 [	Qy 241 GlnSerPheHisLeuAlaLeuLeuArgGlnProGlyIleTyrLysProPheIleIleGly 260		Qy         281 ThrIlePheGluGluAlaLysPheLysAspSerSerLeuAlaSerValValValGlyVal         300           bb         637 ACCATCTTTGAAGAGCCAAGTTCAAGGACAGCAGCCTGGCCTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC	Qy         301 IleGlnValLeuPheThrAlaValAlaAlaLeuIleMetAspArgAlaGlyArgArgLeu 320           Db         697 ATCCAGGTGTTCACAGCTGTGGGGGCTCTCATCATGAAGGAGGCAGGGGGGGTG 756	321 LeuleuValLeuSerGlyValValWetValPheSerThrSerAlaPheGlyAlaTyrPhe

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Squence 29, Application US/10169395

Generace 29, Application US/10169395

GENERAL INPOSTATION

APPLICANT: KATO, Seish

APPLICANT: KATO, Seish

APPLICANT: KATO, Seish

TITLE OF INVENTION: THESE PROTEINS

TITLE OF INVENTION: THESE PROTEINS

FILE REFERENCE: 01997.015100.US

CURRENT APPLICATION NUMBER: US/10/169,395

CURRENT FILING DATE: 2000-01-06

PRIOR FILING DATE: 2000-01-06

PRIOR PRIOR APPLICATION NUMBER: UP 2000-588

PRIOR APPLICATION NUMBER: UP 2000-2299

PRIOR FILING DATE: 2000-01-11

PRIOR PRIOR APPLICATION NUMBER: UP 2000-58367

PRIOR FILING DATE: 2000-01-12

PRIOR FILING DATE: 2000-03-03

PRIOR FILING DATE: 2000-12-28

NUMBER OF SEQ ID NOS: 150

LENGTH: 1461

TYPE: DNA

ONCANISM: Homo sapiens
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Conservative:
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Indels:
Gaps:
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OTHER INFORMATION: n equals
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Best Local Similarity:
Query Match:
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Pred. No.:
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publication US/10169395

publication No. US20040034192A1

GENERAL INFORMATION:

APPLICANT: KATO, Seishi

APPLICANT: KATO, Seishi

APPLICANT: KATO, Seishi

APPLICANT: KIMUTA, TOMOKO

TITLE OF INVENTION: THESE PROTEINS

FILE OF INVENTION: THESE PROTEINS

FILE OF INVENTION: THESE PROTEINS

CURRENT APPLICATION NUMBER: US/10/169,395

CURRENT APPLICATION NUMBER: US/200-585

PRIOR FILING DATE: 2000-01-06

PRIOR FILING DATE: 2000-01-06

PRIOR FILING DATE: 2000-01-01

PRIOR FILING DATE: 2000-01-01

PRIOR FILING DATE: 2000-01-01

PRIOR PLING DATE: 2000-01-01

PRIOR FILING DATE: 2000-01-03

PRIOR PLING DATE: 2000-01-03

PRIOR FILING DATE: 2000-03-03

PRIOR FILING DATE: 2000-12-28

NUMBER OF SEQ ID NOS: 150

SEQ ID NO 19

LENGTH: 789
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Matches:
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1554.50
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67.64%
63.27%
                        ; NAME/KEY: CDS
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US-10-169-395-29
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Query Match:
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Qy         340 eLysLeuThrGlnGlyGlyProGlyAsmSerSerHisValAlaIleSerAlaProValSe 360           bb         715 CAAGCTGACCCAGGGTGCCCTGGCAACTCCTCGCACGTCGCCTCTCTCGGCCCTGTCTC         774           Qy         360 rAlaGlnProVal 364	ANT: Lobashev, A. V. ANT: Lobashev, A. V. ANT: Lobashev, A. V. ANT: Krukovskaya, L. L. OF INVENTION: In silico screening for phenot: OF INVENTION: In silico screening for phenot: T APPLICATION NUMBER: US/10/157,031 T APPLICATION NUMBER: US/10/15/10/15/10/10/15/10/10/10/15/10/10/16/10/10/16/10/10/16/10/10/16/10/10/16/10/10/16/10/10/16/10/10/16/10/10/16/10/10/16/10/10/16/10/10/10/10/16/10/10/10/10/10/10/10/10/10/10/10/10/10/	Pred. No.:   1.01e-92   Length: 2356	15	
Best Local Similarity:         71.51%         Mismatches:         0           Query Match:         51.61%         Indels:         103           DB:         13         Gaps:         1           US-09-886-954A-1         (1-477)         x US-10-169-395-19         (1-789)           QY         1 MetThrProGluAspProGluGluThrGlnProLeuLeuGlyProProGlyGlyGlySerAla         20           Db         1 ATGACGCCCGAGGACACCAGAGGAAACCCAGCCGCTTCTGGGGCCTCCTGGGGCAGCGG         60           QY         21 ProArgGlyArgArgValPheLeuAlaAlaPheAlaAlaAlaLeuGlyProLeuSerPhe         40           Db         61 CCCGGGGGGGGCGCGCCGCCGCCGCCGCGCGCGCGCGC	6.1 AlaProArgleuAspAspAlaAlaAlaAlaBerTrppheGlyAlaValValThrLeuGlyAla 1.8.1 GCCCGGCCTGGACGCCCCCTCTTCTTGGGGGTTCTTGTGACCTTGGGGGTGCC  8.1 AlaAlaGlyGlyValLeuGlyGlyTrpLeuValAspArgAlaGlyArgLysLeuSerLeu 1.8.1 GCGCGGGGGGGGGCGCTGGTGGTGGACCGGCCGGGCGCAAGCTGAGCCTC  1.0.1 LeuLeuCysSerValProPheValAlaGlyPheAlaVallleThrAlaAlaGlnAspVal 1.0.1 LeuLeuCysSerValProPheValAlaGlyPheAlaVallleThrAlaAlaGlnAspVal 1.0.1 TrpMetLeuLeuGlyGlyArgLeuLeuThrGlyLeuAlaCysGlyValAlaSerLeuVal 1.0.1 TrpMetLeuLeuGlyGlyArgLeuLeuThrGlyLeuAlaCysGlyValAlaAsSerLeuVal 1.0.1 TrpMetLeuLeuGlyGlyArgLeuLeuThrGlyLeuAlaCysGlyValAlaSerLeuVal 1.0.1 TrpMetLeuLeuGlyGlyArgLeuLeuThrGlyLeuAlaCysGlyValAlaSerLeuVal 1.0.1 TrpMetLeuLeuGlyGlyArgLeuLeuThrGlyLeuAlaCysGlyValAlaSerLeuVal 1.0.1 TrpMetLeuLeuGlyGlyArgLeuLeuThrGlyLeuAlaCysGlyValAlaSerLeuVal 1.0.1 TrpMetLeuLeuGlyGlyArgLeuLeuThrGlyLeuAlaCygGlyValAlaSerLeuVal 1.0.1 TrpMetLeuLeuGlyGlyArgLeuLeuThrGlyLeuAlaCygGlyValAlaSerLeuVal 1.0.1 TrpMetLeuLeuGlyGlyArgLeuLeuThrGlyLeuAlaCygGlyValAlaSerLeuVal 1.0.1 TrpMetLeuLeuGlyGlyArgLeuLeuThrGlyLeuAlaCygGlyValAlaSerLeuVal 1.0.1 TrpMetLeuLeuGlyGlyArgLeuLeuThrGlyLeuAlaCygGlyValAlaSerLeuVal 1.0.1 TrpMetLeuLeuGlyGlyCortGryC	141 AlaProValTyrIleSerGluIleAlaTyrProAlaValArgGlyLeuLeuGlySerCys [	201 Phemet Produthr Product Pheleuleu Throllo His Argargoling Laborator 201 Phemet Produthr Product Pheleuleu Throllo Hill	DD         658           QY         260 yValSerLeuMetAlaPheGlnGlnLeuSerGlyValAsnAlaValMetPheTyrAlaGl 280           Db         658           QY         280 uThrIlePheGluGluAlaLysPheLysAspSerSerLeuAlaSerValValGlyVa 300           Db         658           QY         300 llleGlnValLeuPheThrAlaValAlaAlaLeuIleMetAspArgAlaGlyArgArgLe 320           Db         658           QY         320 uLeuLeuValLeuSerGlyValValMetValPheSerThrSerAlaPheGlyAlaTyrPh 340           Db         659           CYGGTCTTGTCAGGTGGTCATGGTGTTCAGCACGAGTGCCTTCGGCGCCTACTT 714

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phenotype-associated expressed sequences
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                                                                                                                                                                                    APPLICANT: Van de Vijver, Marc J.
APPLICANT: Van de Vijver, Marc J.
APPLICANT: Bernards, Rene
FILE NEVENTUR. Diagnosis and Prognosis of Breast Cancer Patients
FILE REFERENCE: 9301-188-999
CURRENT APPLICATION NUMBER: US/10/342,887
CURRENT FILING DATE: 2003-01-15
PRIOR PLING DATE: 2001-06-18
PRIOR FILING DATE: 2001-06-18
PRIOR PLING DATE: 2001-06-18
PRIOR PLING DATE: 2002-06-14
PRIOR PLING DATE: 2002-06-14
NUMBER OF SEQ ID NOS: 2699
SEQ ID NO 1685
LENGTH: 2487
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                                                                                                              Linsley, Feter S.
Mao, Mao
Roberts, Christopher J.
Van 't Veer, Laura Johanna
Van de Vliver, Marc J.
                Sequence 1685, Application US/10342887 Publication No. US20040058340A1
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39.01%
                                                                       APPLICANT: Dai, Hongyue APPLICANT: He, Yudong
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ORGANISM: Homo sapiens
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Best Local Similarity:
                                                       GENERAL INFORMATION:
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ValTyrileSerGluileAlaTyrProAlaValArgGlyLeuLeuGlySerCysValGln 162
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                      405 VallysGlyValAlaThrGlyIleCysValLeuThrAsnTrpLeuMetAlaPheLeuVal
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                                                                                       APPLICANT: Mao, Mao
APPLICANT: Roberts, Chris
APPLICANT: Roberts, Chris
APPLICANT: Van t' Veer, Laura
APPLICANT: Bernards, Rene
APPLICANT: Bernards, Rene
TITLE OF INVENTION: Diagnosis and Prognosis of
FILE REFERENCE: 9301-175-99
CURRENT FILING DATE: 2002-06-14
PRIOR APPLICATION NUMBER: 60/380,770
PRIOR PILING DATE: 2002-05-14
NUMBER OF SEQ ID NOS: 2699
CONTRACT OF SEQ ID NOS: 2699
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PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: NM 017585
DATABASE ENTRY DATE: 2001-06-18
    US20030224374A1
Publication No. US20030224374;
GENERAL INFORMATION:
APPLICANT: Dai, Hongyue
APPLICANT: He, Yudong
APPLICANT: Linsley, Peter
APPLICANT: Mao, Mao
APPLICANT: Roberts, Chris
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TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ASSOCIATED WITH TITLE OF INVENTION: PATHWAY
FILE REPERENCE: DO284 NP
CURRENT REPERINCE: DO284 NP
CURRENT FILING DATE: 2004-01-13
PRIOR APPLICATION NUMBER: U.S. 60/440,068
PRIOR PILING DATE: 2003-01-14
PRIOR PLILING DATE: 2003-05-12
NUMBER OF SEQ ID NOS: 823
SOFTWARE: PATENTIN VEXION 3.2
SOFTWARE: PATENTIN VEXION 3.2
SOFTWARE: PATENTIN VEXION 3.2
SEQ ID NO 109
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US-10-755-889-109
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; Publication No. US20040171823A1
; GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
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LENGTH: 2696
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CCCAACTCGCCGCGCTTCCTGCTCTCTCGGGGCAGGGACGAAGAGGCCCTGCGGGGCGCTG 739
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                                                GCCTGGCTGCGTGGACGTCGATGTCCACTGGGAGTTCGAGCAGATCCAGGACAAC
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Publication No. US20030165831A1
GENERAL INFORMATION:
APPLICANT: Lee, John
APPLICANT: Lillie, James
TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
FILE REFERENCE: MRI-006B
CURRENT APPLICATION NUMBER: US/09/814,353
CURRENT APPLICATION NUMBER: US/01-03-21
PRIOR APPLICATION NUMBER: US 60/191,031
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LOCATION: 1, 2525, 2526, 2527, 2528, 2529, 2530, 2531, 2532, 2533,

LOCATION: 2534, 2535, 2536, 2537, 2549, 2540, 2541, 2541, 2542, 2543, 2542, 2541, 2544, 2545, 2546, 2547, 2548, 2559, 2550, 2551, 2552, 2553, 2554, 2554, 2555, 2556, 2557, 2558, 2559, 2560, 2561, 2552, 2553, 20THER INFORMATION: n = A,T,C or G
FEATURE:

NAME/KEY: misc_feature

LOCATION: 2553, 2554, 2555, 2566, 2567, 2568, 2569, 2570, 2571, 2572, 2567, 2581, 2583, 2594, 2559, 2560, 2571, 2572, 2572, 2575, 2575, 2576, 2577, 2578, 2579, 2580, 2581, 2582, 2575, 2576, 2577, 2578, 2579, 2580, 2581, 2582, 2575, 2576, 2577, 2588, 2589, 2590, 2601, 2572, 2576, 2577, 2578, 2578, 2579, 2570, 2571, 2572, 2576, 2577, 2578, 2578, 2579, 2578, 2577, 2577, 2578, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577, 2577,
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Matches:
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PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: US 60/207,124
PRIOR PILING DATE: 2000-05-25
PRIOR PELICATION NUMBER: US 60/211,940
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: US 60/216,820
PRIOR FILING DATE: 2000-07-07
PRIOR PELING DATE: 2000-07-07
PRIOR PELING DATE: 2000-07-25
PRIOR PILING DATE: 2000-07-25
PRIOR FILING DATE: 2000-07-25
NUMBER OF SEQ ID NOS: 22037
SOFTWARE: PASSEQ for Windows Version 4.0
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LOCATION: 2695, 2696
OTHER INFORMATION: n = A,T,C
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A 46		Db 14	, vo	Db 15	RESULT 12 US-10-424-5	; Publicati	; APPLICAN ; APPLICAN ; APPLICAN	; APPLICAN; TITLE OF ; TITLE OF	; FILE REF.	CURRENT HUMBER O SEQ ID NO	TYPE: D		CCATIO  COCATIO  COTHER I	; OTHER I US-10-424-5	nent Mo	Score: Percent Sim	Best Local		ò	3 qu	ò	Db 4	λō	Db 4	Qy	s qa	0,7	9 90	ο <sub>γ</sub>	9 qa
83 GlyGlyValLeuGlyGlyTrpLeuValAspArgAlaGlyArgLySLeuSerLeuLeuLeu 102	355 GGAGGCCTGAGTGCCATGATCCTCAACGACCTCCTGGGCCGGGAAGCTGAGGATCATGTTC 414	CysServalProPheValAlaGlyPheAlaValIleThrAlaAlaGlnAspValTrpMet	TCAGCTGTGCCGTCGGCGGCCGGCTATGCGCTCATGGCGGGTGCGCACGGCCTCTGGATG	123 LeuleuGlyGlyArgLeuleuThrClyLeuAlaCysGlyValAlaSerLeuValAlaTro 142	ValTyrileSerGluIleAlaTyrProAlaValArgGlyLeuLeuGlySerCysValGln	TITITITITI	163 LeuMetValValValGlyIleLeuLeuAlaTyrLeuAlaGlyTrpValLeuGluTrpArg 182 	H-	IGGCTGGCTGTGGCCGGGGGGCGCCTGTGCTCATCATGATCCTGCTGCTCAGCTTCATG	203 Prodluthrepargheleuleulrihrdihilasargargdindlualametalaalaele 222	223 ArgPheLeuTrpGlySerGluGlnGlyTrpGluAspProProlleGly 238	crecereesac	239AlaGluGlnSerPheHisLeuAlaLeuLeuArgGlnProGly1leTyrLys 255	ProPhellelledlyValSerLeuMetAlaPheGlnGlnLeuSerGlyValAsnAlaVal 2		6 MetPheTyrAlaGluThrIlePheGluGluAlaLysPheIysAspSer	955 CTGGTCTACCTGCAGTCCATCTTCGACAGCACCGCTGTCCTGCTGCCCCCCAAGGACGAC 1014	292 SerLeuAlaSerValValValGlyValIleGlnValLeuPheThrAlaValAlaAlaLeu 311 ::: ::: :::	312 IleMetAspArgAlaGlyArgArgLeuLeuLeuValLeuSerGlyValValWetValPhe 331	1066 ACCATGGACTCGCAGGCCGCAAGGTGCTGTTTGGTCTCAGCGGCCATCATTGCT 1125	332 SerThrSerAlaPheGlyAlaTyrPheLysLeuThrGlnGlyGlyProGlyAsnSerSer 351	1126 GCCAACCTGACTCTGGGGGTGTACATCCACTTTGGCCCCCAGGCCTCTGAGC 1176	352 HisValAlaIleSerAlaProValSerAlaGlnProValAsp 365	1177 CCCAACAGCACTGGGGCCTGGAAGCGAGTCCTGGGGGGACTTGGCGCAGCCCTGGCA 1236	366 AlaSerValGlyLeuAlaTrpLeuAlaValGlySerMetCysLeuPheileAlaGly 384	1237 deAccederdederaccite acceptate conference acceptate and defense and defense acceptate and defense acceptate and defense and defense acceptate a	385 PheAlaValGlyTrpGlyProlleProTrpLeuLeuWetSerGlullePheProLeuHis 404	sccardaacraagarccartaacraagacracararardaa	405	1357 GCCCGTGGCGTGGCCTCAGGGCTCTGCGTGGCTGGCTGGC
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Jacation No. US20040031072A1

Ilication No. US20040031072A1

FLICANT: CASOR Thomas Thomas The Licant: Casor Thomas The Licant: Casor Yongwei

TLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With TLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

TRENT APPLICATION NUMBER: US/10/424,599

RRENT FILING DATE: 2003-04-28

MERROR FOR INOS: 285684

ID NO 132422

ID NO 132422

ENGTH: 2202
                                    1475
                                                                                         106 ProPheValAlaGlyPheAlaValIleThrAlaAlaGlnAspValTrpMetLeuLeuGly 125
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46 TyrSerSerProAlalleProSerLeuGlnArgAlaAlaProProAlaProArgheuAsp
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Matches:
Conservative:
Mismatches:
Indels:
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INFORMATION: unsure at all n locations
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SM: Glycine max
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11 Similarity:
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1143 GGAAITITGTICTATTCAACTACCATCTITGCAAATGCAGGAAITICAICCAGCGAAGCT
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GCTGAGATTGCACCTCAAAACTTGAGAGGTGGCCTTGGGTCAGCTGAACCAGCTCTCTGŤŢ
                                               ValValGlyIleLeuLeuAlaTyrLeuAlaGlyTrpValLeuGluTrpArgTrpLeuAla
                                                                                                               1023 GIGGCTICAACGGGAAAAAAGGCTGCAAICCGAITIGCAGAGATCTCAAGAGGAAAAGAIAI
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1425 GTGATT---------GGGTTCTCTAGGTCTGGGACCCATCCCT
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                                                             ValleuGlyCysValProProSerLeuMetLeuLeuLeuMetCysPheMetProGluThr
                                                                                                                                             ProArgPheLeuLeuThrGlnHisArgArgGlnGluAlaMetAlaAlaLeuArgPheLeu
                                                                                                                                                                      CCCAGATGGTTGGCCAAGATGGGGATGATAGATGAGTTTGAGACTTCTTTGCAAGTGTTTA
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RESULT 13

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APPLICANT: Liu, Jingdong
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APPLICANT: Screen, Steven E
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APPLICANT: Tabaska, Jack E
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APPLICANT: Papaska, Jack E
APPLICANT: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5313)B
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 26596
LENGTH: 1797
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US-10-425-114-26596
; Sequence 26596, Application US/10425114
; Publication No. US2004003488BA1
; GENERAL INFORMATION:
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ORGANISM: Oryza sativa
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; OTHER INFORMATION: Clone ID: PAT_MRT4530_62530C.1
US-10-437-963-61061
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Matches:
Conservative:
Mismatches:
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CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 61061
LENGTH: 2003
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ORGANISM: Oryza sativa
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TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21 (53221)B
                                                                                                                                                                                                                                                                                                                                                       976 ATACCGCACACCCCTAATACTAGGAATTGGCCTACTTGTACTGCAACAGCTAAGTGGAAT 1035
                                                                                                                                                                                                                                                                                                                                                                                                                                                            1216 CCTCCTTGCAGTTGCTGTTGTATTTTTCCTC---AAGGATAGCATTTCACAAGATTCTCA 1272
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                                                                                                                                                                                                                                                                                                                          lAsnAlaValMetPheTyrAlaGluThrIlePheGluGluAlaLysPheLysAspSerSe 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              312 eMetAspArgAlaGlyArgArgLeuLeuValLeuSerGlyValValMetValPheSe 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 352 sValAlaIleSerAlaProValSerAlaGlnProValAspAlaSerValGlyLeuAlaTr 372
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 372 pLeuAlaValGlySerMetCysLeuPhelleAlaGlyPheAlaValGlyTrpGlyProil
                                                                                                                          -------GlnSerPheHisLeuAlaLeuArgGlnProGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                332 rThrSerAlaPheGlyAlaTyrPheLysLeuThrGlnGlyGlyProGlyAsnSerSerHi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 eProTrpLeuLeuMetSerGluIlePheProLeuHisValLysGlyValAlaThrGlyIl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    412 eCysValLeuThrAsnTrpLeuMetAlaPheLeuValThrLysGluPheSerSerLeuMe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  452 lLeuPheThrLeuPheCysValProGluThrLysGlyLysThrLeuGluGlnIleThrAl
                            pGlySerGluGlnGlyTrpGluAspProProIleGlyAlaGlu
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US-10-437-963-61061

; Sequence 61061, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Wu, Wei
; APPLICANT: Wu, Wei
; APPLICANT: Barbazuk, Brad
. APPLICANT: Barbazuk, Brad
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1273 CATGTACTACACC----
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Best Local Similarity: 34.19% Mismatches: 182 Query Match: 28.55% Indels: 65 DB: 13 Gaps: 8	A-1 (1-477) × US-10-425-114-24968 (1-2049	Oy 10 GlnProLeuLeuGly	Db 390 AAGCCGCTCATCAACACCGGGAGCTGGTACCGCATGCCGCGGGGGGGG	Qy 23 GlyArg32  Qy 23 GlyArg32	33	510 GCTATCTCGGCCACGCTCTGCACGCTTATTGTCGCGCTAGGTCCCATCCAGTTCGGTTTC	Qy 43 AlaLeuGlyTyrSerSerProAlalleProSerLeuGlnArgAlaAlaProProAlaPro 62	Db 570 ACAIGCGGCTACTCCTCGCCCACGCAGGACGCCATCATTGCTGATCTC 617	63		•	12	Db 738 GCTGCGATTCCAAACATAATTGGGTGGCTCGCGATATCATTGGAAAGATTCCTCTTTC 797	Oy 123 LeuLeuGlyGlyArgLeuThrGlyLeuAlaCysGlyValAlaSerLeuValAlaPro 142	Db 798 TIGITTAIGGGICGGCIGCTAGAAGGAITIGGAGICGTGTAAAIAICGTATACAGTACG 857	143 ValtyrileSerGluileAlaTyrProAlaValArgGlyLeuLeuGlySerCysValGln	828	Oy 163 LeuMetValValValGlyIleLeuLeuAlaTyrLeuAlaGlyTrpValLeuGluTrpArg 182	183 TrpleuAlavalleuGlyCysvallproProSerLeuMetLeuLeumetCysPhemet	978	QY 203 ProGluThrProArgPheLeuLeuThrGlnHisArgArgGlnGluAlaMetAlaAlaLeu 222	3lnGlyTrpGluAspProProileGlyAlaGlu		Qy 241	Db 1143 GAAATAAAGAGATCATTAGCATCGAGGAGGAGGACAACCATAAGGTTCGCTGATATC 1202		1203	00 (	289	Db 1323 ACAAACAGTAATCTAGCAACATTIGGTTTAGGGGCTGTTCAGGTGATTGCTACTGGAGTG 1382
Qy 272 lAsnalaValMetPheTyrAlaGluThrIlePheGluGluAlaLySPheLySAspSerSe 292	292 rLeuAlaSerValValValGlyVallleGlnValLeuPheThrAlaValAlaAlaLeuIl 31	1158	312 eMetAspArgAladJyArgArgLeuLeuLeuValLeuSerGlyValValMetValPheSe	Db 1218 ATTAGACAGAGCCGACGGATCCTCCTTATCATCTCTGCTGGGATGACTCTAĀG 1277 Qy 332 TThrSerAlaPheGlyAlaTyrPheLvsLeuthrGlnGlvGlvProGlvAsnSerKerH 352	1278 CCTCCTTGCAGTTGCTGTTGTATTTTTCCTCAAGGATAGCATTTCACAAGATTCTCA		1335	372	14	н.		Db 1476 IGCGACGCTCGCCAACTGGCTTACATCTTTGGAATAACAATGACAGCAAACTTGAT 1532	Qy 432 tGluValLeuArgProTyrGlyAlaPheTrpLeuAlaSerAlaPheCysIlePheSerVa 452	1533		Db 1593 CGTGTTCGTCATCCTTTGGGTGCCAGAGAAAAGGAAGAACTCTCGAAGAGATACAATG 1652		SULT 15	US-10-425-114-24968 . Sequence 24968 , Application US/10425114 ; Publication No. US20040034888A1	; GENERAL INFORMATION: ; APPLICANT: Liu, Jingdong	APPLICANT: Znou, Inua ; APPLICANT: Kovalic, David K. ; APPLICANT: Screen, Steven B. ; APPLICANT: TALLIN TAL	, AFFLICANT: LADBERA, JACK E. ; APPLICANT: Cao, Yongwei ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules becomisted with	ט ט	CURRENT APPLICATION NUMBER: US/10/425,114; CURRENT FILING DATE: 2003-04-28	; NUMBER OF SEQ ID NOS: 73128 ; SEQ ID NO 24968	; LENGTH: 2049 ; TYPE: DNA ; CTANTEN	OKGANISM: Zea mays CAGANISM: Zea mays CAGANISM: Zea mays CAGANISM: Zea mays	; CIHER INFORMATION: Clone ID: LIB3689-227-G11_FLI US-10-425-114-24968	5 Length:	core: ercent Similarity: 51.19%

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AGGTCATTACTCTTGTTATTGTTTCTGTGTCATTTTTTGTGAAGGACAACATAGCTGCT 1502
                                                                                                                    429 SerSerLeuMetGluValLeuArgProTyrGlyAlaPheTrpLeuAlaSerAlaPheCys 448
                                                                                                         369 GlyLeuAlaTrpLeuAlaValGlySerMetCysLeuPheIleAlaGlyPheAlaValGly 388
                                                                     349 AsnSerSerHisValAlaIleSerAlaProValSerAlaGlnProValAspAlaSerVal 368
                                                                                 1503 GGTTGGCACTTATACTCTGTA------
                                    329 MetValPheSerThrSerAlaPheGlyAlaTyrPheLysLeuThrGlnGlyGlyProGly
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Search completed: September 28, 2004, 08:02:21 Job time : 4267 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - nucleic search, using frame\_plus\_p2n model

September 28, 2004, 01:47:14; Search time 2846 Seconds (without alignments) 5005.011 Million cell updates/sec Run on:

1 MTPEDPEETQPLLGPPGGSA......CVPETKGKTLEQITAHFEGR 477 US-09-886-954A-1 **BLOSUM62** 2457 Perfect score: Scoring table: Sequence: Title:

0.5 Xgapop 10.0 , Xgapext Ygapop 10.0 , Ygapext Fgapop 6.0 , Fgapext Delop 6.0 , Delext

55026578 27513289 seqs, 14931090276 residues Total number of hits satisfying chosen parameters:

Searched:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Command line parameters:

-MODEL-frame+ p2n.model -DEV=xlp
-Q=/cqn2 1/USPTO spool p/US0986954/runat 27092004 170632 13400/app\_query.fasta\_1.647
-Q=/cqn2 1/USPTO spool p/US0986954/runat 27092004 170632 13400/app\_query.fasta\_1.647
-DB=EST \_QFWT=fastap = VGFFTX=rst - HINMARTCH=0.1 -LOOPEXX=0
-UNITG=bits -START=1 -END=-1 -MATRIX-blosum62 -TRANS-human40.cdi -LIST=45
-DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFWT=pto -NORM=ext -HEAPSIZE=500 -MINLER=0 -MAXLEN=20000000
-USR=US09886954 @CGN 1 15180 @runat 2709204 170632 13400 -NCPE=6 -ICPU=3
-NO MWAP -LARGEQUERY -NEG SCORES=0 -WAIT - DSPBLOCK=100 -LONGLOG
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

EST:\*

Database

em\_estba:\* em\_esthum:\* em\_esthum:\* em\_estin:\* em\_estmu:\* em\_estro:\* em\_htc:\* gb\_est1:\* em\_estov:\* em\_estpl:\* gb\_est2:\* gb\_htc::\* gb\_est3:\* gb\_est4:\*

em\_estfun:\* em\_estom:\* em\_gss\_hum:\* em\_gss\_inv:\* em\_gss\_pln:\* em\_gss\_vrt:\* em\_gss\_fun:\* 15: 16: 17: 18: 19: 20:

em\_gss\_rod:\*
em\_gss\_phg:\*
em\_gss\_vrl:\*
gb\_gssl:\* em gss mam:\* em\_gss\_mus:\* em\_gss\_pro:\*

29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Score Match Length DB ID  2159 87.9 2101 II AR081806 AK081806 1490.5 60.7 1008 29 AY414180 1485.5 60.7 1008 29 AY414180 1485.5 60.7 1008 29 AY414180 1285.5 60.7 1008 29 AY414180 1285.5 60.7 1008 29 AY414180 1289.5 56.1 1085 12 BM545247 1289 56.1 1085 12 BM545247 1289 56.1 1085 12 BM545247 1289 56.1 1085 12 BM740749 1289 51.6 991 12 BM744230 1289 50.4 889 12 BM744230 1889 12 BM7475409 1899 12 BM744481 1891 50.5 880 12 BM744230 1891 50.1 BM944230 1891 50.1 BM944230 1891 50.1 BM944230 1892 50.1 BM944230 1893 12 BM771736 1894 13 BM944230 1895 60.1 BM9	Score Match Length DB ID  2123 5 87.9 2101 11 AK081806 AK			%				
NO.         Score         Match Length DB         ID           1         2155         87.9         2101         11         AX08100         AX08180           2         1213.5         86.4         1954         11         AX08180         AX414180           4         1490.5         60.7         1008         29         AX414180         AX414180           4         1490.5         60.7         1000         29         AX414182         AX414182           6         1379         56.1         1085         12         BX35379         BX35379         BX35424           1         1379         56.1         1000         29         AX414182         AX414181         AX414181           1         1263         56.2         1000         29         AX414181         AX414181         AX414181           1         1269         56.1         1004         29         AX414181         AX414181         AX414181           1         1269         56.2         1004         29         AX414181         AX414181         AX414181           1         1260         56.2         1004         29         AX414181         AX414181         AX414181         AX414181 </td <td>NO.         Score         Match Length DB         ID         Description           1         2135         87.9         2101         11         AK081906         AK081906           2         2131.5         86.4         1954         11         AK281989         AK2414180           4         1490.5         60.7         1008         29         AK414182         AK414182           4         1490.5         60.7         1008         29         AK414182         AK414182           6         1379         56.1         1006         29         AK414182         AK414181           1         1269         51.7         1008         12         BK454247         AK414181           1         1269         51.6         1000         29         AK414181         AK414181           1         1269         51.6         1004         29         AK414181         AK414181           1         1126         51.6         1004         29         AK414181         AK414181           1         1267         51.6         1004         29         AK414181         AK414181           1         1267         51.6         1004         29         AK4141</td> <td>Result</td> <td></td> <td>Query</td> <td></td> <td></td> <td></td> <td></td>	NO.         Score         Match Length DB         ID         Description           1         2135         87.9         2101         11         AK081906         AK081906           2         2131.5         86.4         1954         11         AK281989         AK2414180           4         1490.5         60.7         1008         29         AK414182         AK414182           4         1490.5         60.7         1008         29         AK414182         AK414182           6         1379         56.1         1006         29         AK414182         AK414181           1         1269         51.7         1008         12         BK454247         AK414181           1         1269         51.6         1000         29         AK414181         AK414181           1         1269         51.6         1004         29         AK414181         AK414181           1         1126         51.6         1004         29         AK414181         AK414181           1         1267         51.6         1004         29         AK414181         AK414181           1         1267         51.6         1004         29         AK4141	Result		Query				
1         2159         87.9         2101         11         AK081806         AK081806           2         123.5         86.4         1954         11         AK7808587         AK281818           1         173.5         60.7         1008         21         AK44180         AK41182           4         1490.5         60.7         1008         22         AK4414182         AK411182           1         1490.5         60.7         1001         23         AK414182         AK414182           1         1440         54.5         932         12         BM45247         BM542247           1         1669         51.6         1008         12         BM44230         BK414181           1         1669         51.7         91         12         BM44230         BM44230         BM44230           1         1669         51.6         80         12         BM44230         BM44230         BM44230           1         168         12         AK414181         CD557801         BM44230         BM44230           1         1241.5         50.2         80         12         BM44230         BM44230           1         123.3         <	1         2159         87.9         2101         11         AK081806         AK081806           2         1215.5         86.4         1954         11         AF28989         AK2414180           4         1405.5         60.7         1008         29         AK414182         AK414182           4         1405.5         60.7         1008         29         AK414182         AK414181           7         1340         54.5         80.2         128         AK414181         AK414181           1         1269.5         51.7         90.1         28         AK414181         AK414181           1         1269.5         51.7         90.1         28         AK414181         AK414181           1         1269.5         51.6         100.4         29         AK414181         AK414181           1         1267         51.6         100.4         29         AK414181         AK414181           1         1267         51.6         100.4         29         AK414181         AK414181           1         1267         51.6         100.4         29         AK414181         AK414181           1         126.2         12.2         14 <td>Q.</td> <td>SCOR</td> <td>Match</td> <td>Length</td> <td>- 1</td> <td>Q</td> <td>scription</td>	Q.	SCOR	Match	Length	- 1	Q	scription
2         2         2         2         2         2         2         2         2         3         AF2895897         AF2895897         AF2814180         AF4814180         AF4814180         AF4814180         AF4814180         AF4814180         AF4814180         AF4814180         AF4814182         AF4814182         AF4814182         AF4814182         AF4814182         AF4814182         AF4814182         AF4814182         AF4814182         AF4814181         AF4814181         AF4814181         AF4814181         AF4814181         AF4814181         AF4814182         AF4814181         AF48141181         AF4814181	2         2         2123.5         86.4         1954         11         AF2895897         AF218180         AF218180         AF2181180         AF2181180         AF21118181         AF2118181		215	7.9	210	11	08180	X081806 Mus mu
3         1113         69.7         1008         29         AY414180         AY414180         AY414181           4         1495.5         60.7         1201         13         BX435379         BX435379         BX435379           5         1485.5         60.7         1201         29         AY414182         BX435379         BX435379           6         1379         56.1         1000         29         AY414182         BX435379         BX435379           1         1293         52.6         830         12         BRA45247         BK4247         BK4247           1         1293         52.6         830         12         BR474181         BK4247         BK4247         BK4247         BK4247         BK4247         BK44287         BK444884         BK444884         BK444884         BK444884         BK444884         BK444884<	3         1113         69.7         1008         29         AY414180         AY414180         AY414181           5         1485.5         60.7         1201         13         BX491579         BX395379           6         1379         56.1         1200         29         AY414182         AY414184           7         1348.5         60.7         120         12         BK45247         BK45247           8         1293         52.6         830         12         BK45247         BK4247           10         56.5         51.7         991         12         BK478832         BK478842         BK478842           11         1267         51.6         830         12         BK471811         AY44181         AY44181           11         1267         51.6         882         12         BK478000         BK478000           12         128         50.1         882         12         BK44181         AY44181           12         128         874         12         BK478000         BK478000           13         128         872         12         BK478000         BK478000           14         123         872         8	73	123.	ė.	95	11	28958	89587 Homo s
4         1490.5         60.7         1201         13 M395379         BX395379           6         1340         56.0         1000         29         AX414182         AX414182           6         1340         54.5         93.2         12         BM545247         BM541242           1         1340         54.5         93.2         12         BM543247         BM5412482           1         1269.5         51.6         93.0         12         BG7700749         BM5414181           1         1269.5         51.6         1004         29         AX44181         CD55401         BM5414181           1         1269.5         51.6         1004         29         AX44181         CD54414181           1         1269.5         51.6         1004         29         AX4414181         CD54414181           1         126.6         51.6         1004         29         AX4414181         CD54414181           1         12.2         51.6         1004         29         AX4414181         CD54414181           1         12.2         51.6         1004         29         AX4414181         CD54414181           1         10.2         12.8	4 1490.5         60.7         1201         13 RX395379         BX395379         BX395379           6 1379         56.5         1008         12         BX44182         BX4412182           1 140         54.5         930         12         BK478247         BK4412182           1 140         54.5         931         12         BK47842         BK441181           1 153         52.6         830         12         BK47842         BK441181           1 169         51.7         991         12         BK44181         BK44181           1 10         166         51.6         1004         29         AY414181         BK44181           1 10         166         55.6         880         12         BK47842         BK44181           1 12         166         156         1004         29         AY414181         BK44181           1 12         168         12         BK478624         BK44181         BK44181           1 12         168         12         BK478624         BK44181         BK441481           1 12         168         12         BK44181         BK441481         BK441481           1 12         168         12         BK	٣	171	ė,	8	59	11418	14180 Homo s
5         1485.5         60.5         1000         29         AV414182         AV441182         AV4414181           7         1340         54.5         1000         29         AV414181         BM545247         BM545247           8         1269.5         51.0         80         12         BG479042         BM545247         BM545247           10         1269.5         51.7         90         12         BG470043         BM545247         BG4700443           11         1267.5         51.6         875         14         CD557801         CD557801         BG4700403           12         1241.6         50.5         80         12         BG470043         BM444230         BM444230         BM44430         BM44414481           13         1241.6         50.5         80         12         BM444230         BM44430         BM44430         BM44430         BM44430         BM44430         BM444430         BM44430         BM44430         BM44430         BM44430         BM44430         BM444430         BM444430         BM444430         BM44444         BM444430         BM444430         BM444430         BM444430         BM444430         BM444430         BM444430         BM444430         BM444430         BM44	5         1485.5         60.5         1000         29         AV4414182         AV4414182           6         1379         54.5         1006         12         BM545247         BM545247           7         1340         54.5         1006         12         BG4700449         BM545247         BM545247           1         1269         51.6         93         12         BG4700449         BM545247         BM545247           1         1269         51.6         93         12         BG4700429         BG700449           1         1269         51.6         87         14         BM545247         BG70443         BG70443           1         1         1269         51.6         80         12         BG4700423         BG74144181         CD557801           1         1         1241         80         12         BG471830         BG471800         BG471800         BG471800           1	4	490.	ö	2	13	39537	95379 BX3953
6         1379         56.1         1085         12         BM545247         BM545247           8         1240         56.1         1085         12         BG479842         BM545247           9         1269.5         51.7         99.1         12         BG470749         BG470749           10         1269.5         51.7         99.1         12         BG470749         BG4707441           11         1267         51.6         875         14         CD557801         BM64430         BM64430           12         1241.5         50.5         88         12         BG700749         BG717034           13         123         50.2         77         12         BM64230         BM64430         BM64430           14         123         50.2         77         12         BM74430         BM74430         BM74430           15         123.0.5         50.1         88         12         BM74430         BM74430         BM74430           16         118         18         12         BM71034         BM74430         BM74430         BM74430           17         18         12         12         14         CD55400         BM744141	6         1379         56.1         1085         12         BM545247         BM545247           8         1240         54.5         932         12         BG479842         BG479842           1         1240         54.5         932         12         BG470449         BG4700449           1         1269.5         51.7         991         12         BG700749         BG44780           1         1267         51.6         6104         29         AX414181         CD557801           1         1267         51.6         87         12         BG700749         BG44230           1         1267         51.6         87         12         BG7007443         BG444230           1         1233         50.2         40.4         CD557801         BG444230         BM44230           1         1220.5         80         12         BM44230         BM44230         BM44230           1         123.0         50.1         80         12         BG717034         BG444230           1         123.0         50.1         80         12         BG717034         BG444230           1         1         1         1         1	5	485.	ö	8	29	41418	14182 Mus mu
7         1340         54.5         932         12         B6479842         B6479842         B64700449           9         1269.5         51.6         104         29         A7444181         A7444181           10         1269         51.6         104         29         A7444181         BG700749           11         1269         51.6         104         29         A7444181         A7444181           12         1241.5         50.5         880         12         BG7007430         BR044230         BG7448101           14         1238         50.4         828         12         BG478000         BG448000         BG448000           14         1238         50.4         828         12         BG478000         BG448000         BG448000           14         1236         80.1         12         BT77409         BG717034         B	7         1340         54.5         932         12         BG479842         BG479842         BG470849           9         1259         52.6         830         12         BG479842         BG4700749           10         1269         51.6         991         12         BI334832         BY444181           11         1269         51.6         1004         29         R744181         R7444181           12         1241.5         50.5         880         12         BN044230         BG47400           14         123         50.4         828         12         BM044230         BG444280           14         123         50.2         880         12         BM044230         BG44480           15         123         50.2         880         12         BM044230         BG444280           16         123         50.1         88         12         BG471034         BG744280           17         18         183         12         BG771734         BG771734         BG771734           18         18         12         BG771734         BG771734         BG771734         BG771774           18         18         12 <t< td=""><td>9</td><td>37</td><td>Ġ</td><td>8</td><td>12</td><td>54524</td><td>15247</td></t<>	9	37	Ġ	8	12	54524	15247
B         1293         52.6         830         12         BG700749         BG700749           10         1269         51.7         991         1269         51.7         991           11         1269         51.6         875         14         CD57801         BM044230         BM044230           13         1238         50.5         880         12         BM044230         BM044230         BM044230           14         1233         50.2         880         12         BG717034         BM044230         BM044230           14         1233         50.2         777         12         BG717034         BM044230         BM044230           14         1233         50.2         49.8         BG478000         BG478000         BG747004           15         1222.5         49.8         BG471704         BG717034         BG717034         BG717034           16         1222.5         49.8         BG3         12         BG717034         BG717034           17         1193.5         48.6         B3.8         12         BG7171736         BG717174           18         1119         45.6         89.1         12         BB182865         BB1828676<	B         1293         52.6         830         12         BG700749         BG700749           10         1269.5         51.7         12         BG700749         BG700749           11         1269.5         51.7         104         29         AY414181         CD57801           12         1241.5         51.6         1004         29         AY414181         CD57801           13         1238         50.6         875         14         CD557801         BM044230           14         1238         50.2         877         12         BG717034         BG7478000           16         1230.5         48.6         838         12         BG7817034         BG7471736           17         1230.5         48.6         838         12         BG7817736         BG7771736           18         1220.5         48.6         838         12         BG781773         BG717736           19         1120.5         45.6         894         13         BG791177         BG791177           11         45.6         894         13         BG791177         BG7917173           20         1116         45.6         894         13         BG79186	7	34	₩.	<b>(1)</b>	12	47984	79842
9         1269.5         51.7         991         12         B134832         B134832         B134832           10         1269         51.6         1004         29         AY414181         CD554801         CD554801           11         1267         51.6         1004         29         AY414181         CD554801         CD554801           12         1241.5         50.5         880         12         BM044230         BG478000         BG471004           14         1238         50.0         48.9         12         BG71034         BG71074         BG45000           15         1230.5         50.1         889         12         BG771736         BG771774         BG771777	9         1269.5         51.7         991         12         B134832         B134832         B134832           11         1267         51.6         1004         39         AY414181         CD557801         CD557401           12         1241.5         50.5         880         12         BM44230         BG478000         BG478000         BG478000           14         1233         50.1         889         12         BA771034         BG717034         BG777034         BG777034 <td>8</td> <td>129</td> <td>ď</td> <td>(T)</td> <td>12</td> <td>70074</td> <td>00749</td>	8	129	ď	(T)	12	70074	00749
10         1269         51.6         1004         29         AV4414181         AV4414181         AV4414181           11         1241.5         51.6         880         12         BM44230         BM644230	10         1269         51.6         1004         29         AV4414181         AV4414181         AV4414181           11         1267         51.6         879         12         BA771034         BM044230         BM044136         BM14460         BM14460         BM14460         BM14460         BM14460         BM14460         BM	σ	269.	ä	6	12	33483	34832
11         1267         51.6         875         14         CD557801         CD557801           13         1238         50.5         880         12         BM044230         BM044230           14         1238         50.6         12         BM044230         BG478230           14         1233         50.2         777         12         BG717034         BG717034           15         1222.5         49.6         838         12         BG771736         BG7717736           16         1222.5         48.6         838         12         BG771777         BG771776           18         116         45.4         89.1         12         BG281777         BG717777           18         116         45.4         89.1         12         BI144765         BG2817777           20         1119         45.5         89.1         12         BI144765         BG2817777           21         116         45.4         85.4         12         BI146408         BI114765         BG2817777           22         1116         45.4         85.4         12         BI146408         BI114765         BG2817777           23         1074.5         4	11         1267         51.6         875         14         CD557801         CD557801           13         1238         50.5         880         12         BM044230         BM044230           14         1238         50.6         880         12         BM044230         BG478000           14         1238         50.2         877         12         BG771736         BG771736           16         1222.5         49.6         838         12         BG281777         BG771736           11         1193.5         48.6         894         12         BG771736         BG21177           11         45.6         894         13         BG11865         BG21177         BG71174           20         1119         45.6         894         13         BG11865         BG21177           21         1016         45.4         813         12         B128656         B114765           22         1016         45.4         813         12         B128656         B128656         B128656           23         1074.5         43.7         1002         12         B1818686         B1818656         B18186659           24         43.9	10	56	ä	0	29	418	14181
12         1241.5         50.5         880         12         BM044230         BM044230         BM044230           14         1238         50.4         889         12         BG478000         BG478000           14         1233         50.4         889         12         BT57409         BG771736         BG771736           15         1230.5         50.1         889         12         BT757409         BG771736         BG7717476	12         1241.5         50.5         880         12         BM044230         BM044230           14         1238         50.4         88         12         BG478000         BG478000           14         1233         50.4         88         12         BG71034         BG71034           15         1230.5         50.1         88         12         BT757409         BG71736           16         123.5         48.6         89         12         BT77136         BG717736         BG717736           11         48.6         89         12         BT771736         BG717777         BG717774           11         45.6         894         13         BG114765         BG211777         BG717774           21         1116         45.4         854         12         BG717777         BG717774         BG717776           21         1116         45.4         854         12         BG7186         BG7117476           22         1074         5         43.3         813         12         BR78666         BG717476           23         1074         5         43.1         813         12         BG78966         BG73767           <	11	126	ä	r	14	3780	57801
13         1238         50.4         828         12         B6478000         BG471034         BG717034           14         1230.5         50.1         89         12         B647800         BG717034           15         1230.5         49.8         89         12         BG7217034         BI771736           16         1222.5         49.8         879         12         BG771736         BG771736           18         113         48.6         838         12         BG281777         BG281777           18         1120.5         48.6         894         13         BG281777         BG281777           19         1120.5         48.6         894         13         BG281777         BG281777           20         1119         45.5         899         12         B1916408         B1114765           21         1076         43.8         813         12         B1828949         B18114765           22         1076         43.9         1002         12         B1828949         B1828949         B1828949           24         10.0         12         B1828949         B1828949         B1828949         B1828949           25         <	13         1238         50.4         828         12         B6478000         BG478000         BG478000           14         1233         50.2         77         12         BG717034         BG717034           15         1230.5         50.1         879         12         BG771736         BG717034           16         1222.5         49.8         879         12         BG771736         BG717034           17         1193.5         48.6         889         12         BG731777         BG717736           18         120.5         48.6         894         13         BO919165         BG7171736           19         45.4         894         13         BO919165         BG7171736           20         1116         45.4         894         13         BO919165         BG7114765         BG7114765           21         110         45.4         894         13         BO919165         BG7114765         BG7114765           22         1076         43.8         813         12         BG82849         BIS31908         BIS31908         BIS31908         BIS311908         BIS311908         BIS311908         BIS311908         BIS311908         BIS311908         BI	12	241.	ö	œ	12	1423	14230
14         1233         50.2         777         12         B6717034         BG717034         BG717034           16         1220.5         49.6         89         12         B1757409         B1757409           16         1220.5         48.6         89         12         BG717176         BG71777           18         18.5         48.6         89         12         BG71777         BG281777           18         18.6         89         12         B114765         BG281777         BG281777           19         45.6         89         12         B172465         BG281777         BG281777           20         1119         45.6         89         12         B1828656         BG281777         BG281777           21         116         45.4         854         12         B1828656         BG281749         BG2818656         BG281876           23         1074.5         43.7         1002         12         B18286549         BI8388656         BI83886549         BI83886654         BI8388665         BI8388674         BI8388665         BI8388665         BI8388665         BI8388674         BI8388674         BI8388674         BI8388674         BI8388674         BI8388674	14         1233         50.2         777         12         B6717034         BG717034         BG717034           15         1222.5         49.6         838         12         B777409         B1757409         B1757409           16         1222.5         49.6         838         12         BG71736         BG71774           17         1193.5         48.6         89.1         12         B114765         BG71777         BG781777           18         1120.5         45.6         89.1         12         B1114765         BG717177         BG781777           20         1116         45.4         85.4         12         B176408         B171777         BG781777           21         116         45.4         85.4         12         B176408         B171777         BG781777           22         1074.5         43.7         1002         12         B176408         B18174765         BG79176177           23         1074.5         43.7         1002         12         B18186658         B181828649         B181828649<	13	23	ö	CA	12	800	78000
15         1230.5         50.1         889         12         BT757409         BT757409           16         1222.5         48.6         879         12         BT771736         BT77740           17         183.5         48.2         80.1         12         BT114765         BG281777           18         1183.5         48.2         80.1         12         BT114765         BG281777           20         111.6         45.5         89.9         12         BT114765         BD3114765           21         111.6         45.4         89.4         13         BO19165         BD3114765           21         111.6         45.4         89.4         13         BO19165         BD3114765           22         111.6         45.4         89.4         12         BT818656         BD311476           23         10.7         13         BO20949         BD31828656         BD31828656         BD31828656           24         10.5         41.9         773         13         BO603775         BD31828658         BD31828658           25         10.3         64.1         13         BO808346         BD31828658         BD31828658           26         <	15         1230.5         50.1         889         12         BT757409         BT757409           16         1222.5         48.6         879         12         BG771736         BG771736           11         48.6         89.8         12         BG771736         BG781777           18         1183.5         48.6         894         13         BG0319165         BG281777           20         111.9         45.6         894         13         BG019165         BG281777           21         111.6         45.4         894         13         BG019165         BG2817476           21         111.6         45.4         894         13         BG019165         BG2114765           21         111.6         45.4         894         13         BG18666         BI5114765           22         1074.5         43.8         813         12         B1828696         BI518166         BI518166           24         1059         43.1         813         12         B1828699         BI518166         BI5181666           25         1036.5         41.9         773         13         B0603775         B0603775         B0603775           26	14	123	ö		12	703	17034
16         122.5.         49.8         879         12         B6771736         BG771736           17         1193.5.         48.6         838         12         BG781777         BG281777           18         1183.5.         48.6         838         12         BG281777         BG281777           18         1120.5         45.6         894         13         BG919165         BG2819165           20         1119         45.5         899         12         B1916408         B1828949           21         1106         43.8         813         12         B1828949         B1828949           23         1074.5         43.7         1002         12         B1828949         B1828949           24         1055         42.9         700         13         BD4009572         BG1099572           25         1036.5         42.9         700         13         BG200775         BG1099572           26         1036.5         42.2         93         10         BE986058         BE910478           27         1030.5         41.3         62.1         10         BE986074         BE90077107           28         980         39.6 <td< td=""><td>16         122.5.         49.8         879         12         B6771173         BG281777         BG281777           11         1183.5.         48.6         834         12         B6771173         BG281777         BG281777           18         1183.5.         48.6         894         13         BG919165         BG18177         BG18177           19         45.6         894         13         BG19165         BG2919165         BG1919165           20         1116         45.4         85.4         12         B1916408         BG2919165         BG2919165           21         1116         45.4         85.4         12         B1916408         BG2919165         BG2919165           22         1076         43.8         813         12         B1828656         BG2919166         BG2919166</td><td>15</td><td>30.</td><td>ö</td><td>œ</td><td>12</td><td>740</td><td>57409</td></td<>	16         122.5.         49.8         879         12         B6771173         BG281777         BG281777           11         1183.5.         48.6         834         12         B6771173         BG281777         BG281777           18         1183.5.         48.6         894         13         BG919165         BG18177         BG18177           19         45.6         894         13         BG19165         BG2919165         BG1919165           20         1116         45.4         85.4         12         B1916408         BG2919165         BG2919165           21         1116         45.4         85.4         12         B1916408         BG2919165         BG2919165           22         1076         43.8         813         12         B1828656         BG2919166	15	30.	ö	œ	12	740	57409
17         1193.5         48.6         838         12         BG281777         BG281777           18         1183.5         48.6         894         13         BG281777         BG281777           19         45.6         48.6         894         13         BG919165         BG281777           20         1119         45.6         899         12         BIG18656         BG319166           21         1076         48.4         85.4         12         BIG28656         BIG31908           23         1076.5         43.7         1002         12         BIG28656         BIG31908           24         1059         43.1         833         12         BIG28659         BIG31908           25         1036.5         42.2         934         10         BD310479         BC30909           26         1036.5         42.2         934         10         BD310479         BC400977           26         1036.5         42.2         934         10         BD300874         BC400977           27         1030.5         41.9         773         13         BG60375         BC400977           28         948         38.6         21.2	17         1193.5         48.6         838         12         BG281777         BG281777         BG281777           18         1128.5         48.6         894         13         BG281777         BS114765         BS114765           20         1119         45.5         899         12         B1916408         BIS131908         BIS131908           21         1116         45.4         85.4         12         B1828656         BIS31908         BIS31908           23         1074.5         43.7         1002         12         B1828649         BIS31908	16	22.	φ.	~	12	1173	71736
18         1183.5         48.2         801         12         B1114765         B0114765           19         1120.5         45.6         894         13         B0219165         B0219165           20         1116         45.6         894         13         B0219165         B1919169           21         1116         45.4         85.4         12         B1828699         B1828656           23         1074.5         43.7         80.2         1833         12         B1828949         B18281998           24         1055         42.9         70.0         13         B1828949         B18281949         B18281949           25         1074.5         43.1         80.1         12         B1828949         B18281949         B18281949           26         1055         42.9         70.0         13         B1828949         B18281949         B18281949           27         1036.5         42.9         70.0         13         B1828949         B1818126390           27         1036.5         42.9         773         13         B0603775         B20106572           28         990         40.3         64         10         B1886058         B1826	18         1183.5         48.2         801         12         B1114765         B0114765           19         1120.5         45.6         894         13         B0219165         B0219165           20         1116         45.4         894         13         B0219165         B1014769           21         1116         45.4         894         13         B101696         B1031908         B1828656           22         1076         43.8         813         12         B1828694         B18131908         B1828694           24         1059         43.1         833         12         B1826390         B1828694           25         1055         42.9         70         13         B0109572         B1828634           25         1056         41.9         773         13         B0603775         B1828634           26         1036.5         41.9         773         13         B0603775         B0109570           27         1030.5         41.9         773         13         B0603775         B0200374           28         90         40.3         664         10         BB986058         B0200036           29         41	17	93.	œ.	സ	12	1177	BG281777
19         1120.5         45.6         894         13         BO919165         BO919165         BO919166           20         1116         45.4         899         12         B1716408         B1914408         B1914408           21         1116         45.4         813         12         B1828656         B1831908         B1831908           22         1074.5         43.7         1002         12         B1828649         B18281908         B18281908         B18281908         B18281908         B18281908         B18281908         B18281908         B18281908         B18281909         B18281009         B18281009 <td>19         1120.5         45.6         894         13         BO919165         BO919166           20         1119         45.4         894         12         B1916408         B1916408         B1916408           21         1116         45.4         813         12         B1916408         B1916408         B1916408           22         1076         43.8         813         12         B1828656         B18286949         B18281908           24         1059         42.2         9         700         12         B1828949         B1828949         B1828949           25         1055         42.9         700         13         B0109572         B18288949         B18288949           26         1055         42.9         700         13         B0109572         B20109572           26         1055         42.9         700         13         B0109572         B20109572           27         1030.5         40.3         664         10         B18986074         B1808074         B182986074           30         40.3         664         10         B18986074         B182986074         B182986074         B182996089           31         40.4</td> <td>18</td> <td>83.</td> <td>œ,</td> <td>0</td> <td>12</td> <td>476</td> <td>BI114765</td>	19         1120.5         45.6         894         13         BO919165         BO919166           20         1119         45.4         894         12         B1916408         B1916408         B1916408           21         1116         45.4         813         12         B1916408         B1916408         B1916408           22         1076         43.8         813         12         B1828656         B18286949         B18281908           24         1059         42.2         9         700         12         B1828949         B1828949         B1828949           25         1055         42.9         700         13         B0109572         B18288949         B18288949           26         1055         42.9         700         13         B0109572         B20109572           26         1055         42.9         700         13         B0109572         B20109572           27         1030.5         40.3         664         10         B18986074         B1808074         B182986074           30         40.3         664         10         B18986074         B182986074         B182986074         B182996089           31         40.4	18	83.	œ,	0	12	476	BI114765
20         1119         45.5         899         12         BI916408         BI916408         BI916408           21         1116         43.4         854         12         BI828656         BI838656         BI838656           23         1076.5         43.8         83.1         BI828656         BI838656         BI838656           24         1059         43.1         83.3         12         BI8286949         BI828649           25         1055         42.2         934         10         BI9210478         BI8286949           26         1055.5         42.2         934         10         BI9210479         BI9286949           27         1030.5         41.9         673         10         BI9310479         BI9286949           29         10         BI9310479         BI9386074         BI9386074         BI9386074           30         948         39.6         621         10         BI9386074         BI9386074           31         948         38.6         212         II ARK08946         AK089946           32         948         38.6         212         II ARK0966         BI9007581           33         947.5         38.6	20         1119         45.5         899         12         BI916408         BI916408         BI916408           21         1116         45.4         85.4         12         BIR28656         BI828656         BI828656           23         1076         43.4         85.4         12         BI828656         BI828656         BI828656           24         1059         43.7         1002         12         BI8286949         BI8286949         BI8286949           24         1059         43.1         833         12         BI828699         BI8286949         BI8286949           25         1055         42.2         934         10         BI926699         BI9286949         BI8286949         BI8286949           26         1036.5         42.2         934         10         BI926698         BI9269949         BI8286949         BI9286949         BI9286949         BI9286949         BI9286949         BI9286949         BI9286949         BI9286949         BI9286949         BI9286949         BI9286968         BI9286968         BI92869949         BI9286968         BI92869949         BI92869949         BI92869949         BI92869949         BI92869949         BI9286999         BI92869949         BI92869949         BI9286994 <td>19</td> <td>20.</td> <td>ın.</td> <td>ത</td> <td>13</td> <td>916</td> <td>9165</td>	19	20.	ın.	ത	13	916	9165
21         1116         45.4         46.4         12         B1828656           23         1076.5         43.8         813         12         B1821908         B1831908           24         1059         43.1         813         12         B1821908         B182191908           24         1059         43.1         833         12         B1828949         B182191908           25         1036.5         42.9         700         13         BQ109572         BC828390           26         1036.5         42.9         700         13         BQ109572         BC8100473           28         990         40.3         664         10         BE986058         BE910478           29         30         41.9         773         13         BQ603775         BE986058           29         40         39.6         41.0         BE986058         BE986058         BE986078           30         973         39.6         920         10         BE986058         BC80603775           31         948         38.6         64.10         BE986058         BC806058         BC806058           32         64         10         BE986058         BC806	21         1116         45.4         854         12         BI828656           22         1076         43.8         813         12         BI831908         BI831908           23         1074.5         43.8         813         12         BI821908         BI8281908           24         1059         43.1         813         12         BI828949         BI8281908           25         1055         42.9         70         13         BC109572         BC2010478           26         1036.5         41.9         773         13         BC603775         BC109572           28         990         40.3         664         10         BE986058         BC601375           29         973         39.6         920         10         BE986058         BC601375           31         947.5         36.4         10         BE986058         BC601375         BC601375           31         947.5         36.4         10         BE986058         BC601375         BC601375           31         947.5         38.6         64.1         BC70107         BC70107         BC70107           32         38.6         68.4         12         BC70107<	20	111	ın.	ത	12	640	6408
22         1076         43.8         813         12         B1831908         B1831908         B1831908           23         1074.5         43.7         1002         12         B1828949         B1828949         B1828949           24         1055         42.9         700         13         B1828949         B1828949         B1828949           25         1055         42.9         700         13         B0109572         B0109572           26         1036.5         42.2         74         10         B1828049         B1828949         B1828949           27         1036.5         42.2         70         13         B0109572         B0104778         B0210478           28         1036         40.3         664         10         B1896058         B1896054         B1896054         B1896054           30         94         38.6         671         10         B1896074         B1896074         B1896074         B1896074         B1896074         B1996074         B1996074         B1996074         B1996074         B19960776         <	22         1076         43.8         813         12         B1831908         B1831908         B1831908           24         1059         43.1         10         212         B1828949         B1828949         B1828949           24         1059         42.2         70         13         B1010572         B1828949         B1828949           25         1055         42.9         70         13         B0109572         B2828949         B1828949           26         1055         42.9         70         13         B0109572         B2828949         B1828949           27         1030.5         41.2         734         10         B1928949         B1828949         B1828949           26         1030.5         41.2         734         10         B1926979         B0109572         B0109572           27         1030.5         40         38.6         41         B18986074	21	17	10	டம	12	865	8656
23         1074.5         43.7         1002         12         BI828949         BI828949           24         1059         43.1         833         12         BI826390         BI826390           25         1055         42.1         83.1         2         BI826390         BI826390           26         1055         42.2         93.4         10         BE910478         BI826390           27         1030.5         41.9         773         13         BO603775         BC910478           29         980         39.9         62.1         10         BE986074         BE986058           30         973         39.6         62.1         10         BE986074         BE986058           31         978         39.6         62.1         10         BE986074         BE986058           32         948         38.6         67.7         11         AK09246         AK089246           33         947.5         38.6         67.7         12         BC9070107         BC9070107           34         38.6         68.4         12         BT90761         BC9044799         BC944799           35         38.0         20.8         11	23         1074.5         43.7         1002         12         BI826390         BI828949           24         1059         42.1         833         12         BI826390         BI826390           25         1055         42.1         833         12         BI826390         BI826390           26         1055         42.2         934         10         BE910478         BE920478           27         1030.5         41.9         773         13         B6603775         BE910478           29         940         39.9         621         10         BE986058         BE96058           30         973         39.6         621         10         BE986054         BE986058           31         948         39.6         621         10         BE986054         BE986058           31         973         39.6         621         10         BE986054         BE986058           31         948         38.6         621         10         BE986054         BE996058           32         621         10         BE908446         BE908058         BE908058           33         947.5         38.6         684         12	22	07	Ψ.	$\overline{}$	12	190	1908
24         1059         43.1         B1826390         B1826390           25         1055         42.9         700         13         BQ109572         BC109572           26         1036.5         42.9         700         13         BQ109572         BC109572           28         42.9         70         13         BC0603775         BC109572         BC109572           28         990         40.3         664         10         BE986058         BC003775           30         973         39.6         920         10         BE986054         BC603775           31         948         38.6         624         10         BE986054         BC603775           31         948         38.6         624         10         BC90446         BC603775           33         947.5         38.6         684         12         BC707107         BC707107           34         938         38.2         735         1         AK089246         AK089246           34         938         38.2         735         1         AK089246         AK089246           34         938         38.2         735         1         AK089246         A	24         1059         43.1         B1826390         B1826390           25         1055         42.2         700         13         BQ109572         BC109572           26         1036.5         42.9         700         13         BQ109572         BC109572           26         1036.5         42.9         700         13         BQ109572         BC1040572           28         990         40.3         664         10         BE986058         BC201075           30         973         39.6         920         10         BE986054         BC603175           31         949         38.6         920         10         BE986054         BC603175           31         949         38.6         62.1         1         BC603106         BC603175           34         948         38.6         684         12         BC707107         BC707107           34         938         38.2         735         12         BC604799         BC644799           35         93.1         37.9         994         13         BC644799         BC644799           36         35.2         683         10         BC644739         BC644799 </td <td>23</td> <td>074.</td> <td>æ.</td> <td>8</td> <td>12</td> <td>894</td> <td>8949</td>	23	074.	æ.	8	12	894	8949
25         1055         42.9         700         13         BQ109572         BQ109572           26         1036.5         41.2         934         10         BE910478         BE910478           27         1030.5         41.2         934         10         BE986058         BG6030475           28         990         40.3         664         10         BE986054         BG603047           30         973         39.6         920         10         BF9086074         BE986078           31         943         38.6         64         10         BF9086074         BE986078           31         943         38.6         67         11         BE9086074         BE986079           32         947.5         38.6         684         12         BK089246         BK089246         BK089246           34         948         38.6         684         12         BK008943         BK099246         BK099246           34         938         38.2         735         12         BK008943         BK008943         BK008943         BK008943           36         931         37.9         994         13         BK75028         BK044156      <	25         1055         42.9         700         13         BQ109572         BQ109572           26         1036.5         42.2         734         10         BE910478         BE910478           27         1030.5         41.2         734         10         BE986058         BB960375           29         990         40.3         664         10         BE986074         BE986058         BE986078           30         973         39.6         920         10         BE986074         BE986078         BE986078           31         949         621         10         BE986074         BE986074         BE986078           32         973         39.6         671         10         BE986074         BE986074           33         947.5         38.6         677         12         BR707107         BR9707107           34         938         38.6         677         12         BR707107         BR9707107           35         93.1         38.2         735         12         BM008943         AK079650         AK079650           36         93.1         11         AK079650         AK079650         BK750238         BK750238	24	05	ω.	83	12	633	6390
6         1036.5         42.2         934         10         BE910478         BE910478         BE910478           7         1030.5         41.9         773         13         BG603775         BG86053           9         980         39.9         621         10         BE986058         BE986074           9         99.9         621         10         BE986074         BE986074           9         93.9         621         10         BF308306         BE986074           1         38.6         67.7         12         BG70710.7         BG708246           2         38.6         684         12         BM008943         BG70710.7           3         38.6         684         12         BM008943         BM008943           4         933.5         38.0         2081         11         AK079650         AK079609           5         93.1         37.9         994         13         BQ44799         BG744799           8         88.9         36.2         608         10         BG79217         BG79217           8         88.9         36.2         994         13         BQ44156         BG44156           9 <td>6         1036.5         42.2         934         10         BE910478         BE910478         BE910478           7         1030.5         41.3         764         10         BE986058         BE986058         BE986074           940         39.9         62.1         10         BE986074         BE986074         BE986074           940         39.6         62.1         10         BE986074         BE986074         BE986074           10         39.6         62.1         10         BE986074         BE986074         BE986074           20         39.6         62.1         10         BE986074         BE986074         BE986074           34         38.6         67.7         12         BG707107         BF980836         BF980836         BF980836           38         38.6         67.7         12         BG707107         BR907581         BR907107         BR907107         BR907107           4         38.6         67.8         1         AK079650         BK079670         BK07971070         BK07971070         BK079670         B</td> <td>~</td> <td>0.5</td> <td>ς.</td> <td><math>\circ</math></td> <td>13</td> <td>957</td> <td>9572</td>	6         1036.5         42.2         934         10         BE910478         BE910478         BE910478           7         1030.5         41.3         764         10         BE986058         BE986058         BE986074           940         39.9         62.1         10         BE986074         BE986074         BE986074           940         39.6         62.1         10         BE986074         BE986074         BE986074           10         39.6         62.1         10         BE986074         BE986074         BE986074           20         39.6         62.1         10         BE986074         BE986074         BE986074           34         38.6         67.7         12         BG707107         BF980836         BF980836         BF980836           38         38.6         67.7         12         BG707107         BR907581         BR907107         BR907107         BR907107           4         38.6         67.8         1         AK079650         BK079670         BK07971070         BK07971070         BK079670         B	~	0.5	ς.	$\circ$	13	957	9572
7         1030.5         41.9         773         13         BQ603775         BQ603775           8         990         40.3         664         10         BE986058         BE986058           9         30.3         664         10         BE986058         BE986058           973         39.6         920         10         BF308006         BE386074         BE386078           1         38.6         6212         11         AK089246         BG7070107         BG7070107 <td>7         1030.5         41.9         773         13         BQ603375         BQ603775           8         990         40.3         664         10         BE986058         BE986058           980         39.9         60.3         664         10         BE986058         BE986058           1         36.0         10         BF986058         BE986058         BE986058           1         39.6         92.0         10         BF986074         BE986074         BE986078           1         39.6         92.0         10         BF986074         BF986058         BF986058           3         38.6         684         12         BG707107         BG707107         BG707107           4         38.6         684         12         BG707107         BG707107         BG707107           5         31         37.9         994         13         BQ644799         BG70710           5         31         37.9         994         13         BQ644799         BG7079217           6         6.3         10         BG7079217         BG7079217         BG7079217           8         8         36.6         6.3         10         CA327128<td>26</td><td>036.</td><td>Α.</td><td>m</td><td>10</td><td>047</td><td>.0478</td></td>	7         1030.5         41.9         773         13         BQ603375         BQ603775           8         990         40.3         664         10         BE986058         BE986058           980         39.9         60.3         664         10         BE986058         BE986058           1         36.0         10         BF986058         BE986058         BE986058           1         39.6         92.0         10         BF986074         BE986074         BE986078           1         39.6         92.0         10         BF986074         BF986058         BF986058           3         38.6         684         12         BG707107         BG707107         BG707107           4         38.6         684         12         BG707107         BG707107         BG707107           5         31         37.9         994         13         BQ644799         BG70710           5         31         37.9         994         13         BQ644799         BG7079217           6         6.3         10         BG7079217         BG7079217         BG7079217           8         8         36.6         6.3         10         CA327128 <td>26</td> <td>036.</td> <td>Α.</td> <td>m</td> <td>10</td> <td>047</td> <td>.0478</td>	26	036.	Α.	m	10	047	.0478
8         990         40.3         664         10         BE986058         BE986058           9         39.9         621         10         BE986074         BE986074           9         39.9         621         10         BE986074         BE986074           1         39.9         621         10         BE986074         BE986074           2         34.0         202         10         BF308306         BF308306           3         38.6         674         12         BG707107         BG709346           4         38.6         684         12         BM008943         BR007581           5         33.7         2         BM008943         BM008943           5         38.2         735         12         BM008943         BM008943           5         38.2         735         12         BM008943         BM008943           5         38.2         73         13         BV5007581         BM008943           5         39.1         38.7         38.7         38.7         38.7           6         63.3         13         BV50038         BV75038         BV75038           8         36.2         <	8         990         40.3         664         10         BE986058         BE886058           973         39.9         621         10         BE986074         BE986074           1         39.9         621         10         BE986074         BE986074           1         39.9         621         10         BE986074         BE986074           2         39.9         6212         11         AK089246         AK089246           3         38.6         67.1         12         BG707107         BG707107           3         34.7.5         38.6         68.4         12         BM00843         BR007546           4         33.8         38.2         73.5         12         BM00843         BM008943           5         31.3         38.0         20.8         11         AK079650         BK077107           5         31.1         68.3         13         BY56238         BY750238         BY750238           8         36.6         63.8         10         BB612439         BB612439         BR044156           8         88.5         36.2         90.8         14         CA327128         CA327128           8 <t< td=""><td>27</td><td>030.</td><td>_;</td><td>~</td><td>13</td><td>377</td><td>3775</td></t<>	27	030.	_;	~	13	377	3775
9 980 39.9 621 10 BES86074 BES986074 UI.N 9 93 39.6 621 10 BF308306 BF308306 6018 1 949 38.6 677 12 BG707107 6026 3 947.5 38.6 674 12 BG707107 6026 5 933.5 38.0 2081 11 AK079650 BG64799 BG707107 6026 9 931 37.9 994 13 BO644799 BG7081 BG7081 G036479 9 12.5 37.1 638 13 BY750238 BG7758 BG612439 BG788 G036479 G03666 G038 G0366 G036 G0366 G036 G0366 G036 G0366 G036 G03	980         39.9         621         10         BES86074         BES86074         BES86074         BES86074         BES986074         UI-N           1         949         38.6         6.21         11         AKO89246         AKO89246         MLS           2         948         38.6         6.77         12         BG707107         GOS           3         94.5         38.6         6.84         12         BM008943         AKO9966         BG007107           4         93.5         38.0         2081         11         AKO79650         AKO9969         AKO0969         AKO79650         MLS           5         91.2         37.1         63         13         BV750238         BV750238         BV750239         BV750479         AGE4479	28	ത		CO.	10	605	86058
0         973         39.6         920         10         BP308306         BF308306         6016           1         948         38.6         677         12         BC707107         BC707107         6028           3         94.5         38.6         674         12         BC707107         BC707107         6036           3         94.5         38.6         684         12         BC707107         BC707107         6026           4         938         38.2         735         12         BM00843         BM008943         BC70710         6036           93.1         37.9         994         13         BC644799         BC707965         BC707965         BC707965         BC707965         BC707965         BC707965         BC707965         BC707967	0         973         39.6         920         10         BF308306         6018         BF308306         6018           2         948         38.6         677         12         BG707107         BG708246         AK089246         MNS           3         948         38.6         674         12         BG707107         BG707107         6028           4         938         38.2         735         12         BM008943         BM008943         BG707965         BG707107         6036           931         37.9         994         13         BQ644799         BG7079650         AK079650         AK079650         MNG           7         912.5         37.1         683         13         BY750238	29	æ	ď.	$\sim$	10	607	36074 UI-N
1         949         38.6         2125         11         AK089246         AK08922312         AK08922312	1         949         38.6         2125         11         AK089246         AK089246         AK089246         Mus           2         948         38.6         677         12         BG701107	30	7	Ψ.	92	10	830	38306 6018
2         948         38.6         677         12         BG707107         6           3         947.5         38.6         684         12         B1907581         B1907581           938         38.6         684         12         B1907581         B1907581           5         38.0         2081         11         AK079650         AK079650           6         931         37.9         994         13         B0644739         B0644799           8         900         36.6         638         10         B8612439         B8644799         B750238           9         36.2         608         10         B679217         B6679217         CA327128           8         36.2         908         10         B679217         CA327128         B679217           8         36.2         908         10         A679217         B74156         B744156           8         869         35.4         13         B0944156         B1402088         B1402088           8         839         34.1         917         10         B740667         CB866069           8         84.1         94         14         CA322132         CA322312<	2         948         38.6         677         12         BG707107         BG70707	31	₹*	m.	12	11	924	39246 Mus
3 947.5 38.6 684 12 B1907581 B1907581 81907581 8 933.5 38.0 2081 12 AK079650 AK079650 AK079650 AK079650 B23.5 38.0 2081 12 AK079650 B0644799 B064799 B064799 B064799 B064799 B064799 B064799 B064799 B064799 B064799 B0679979 B079979 B07999 B079979 B0799979 B07999 B0799979 B0799979 B07999 B07999 B07999 B07999 B07999	3 947.5 38.6 684 12 B1907581 B1907581 8  4 938 38.2 735 12 BM008943 BM0089439 BM008943 BM008944 BM0008944 BM008944 BM0008944 BM0008944 BM0008944 BM0008944 BM0008944 BM0008944 BM008944 BM0008944 BM00089	32	94	m.	~	12	710	07107 6026702
4         938         38.2         735         12         BM0008943         BM0008943         BM0008943         BM0008943         BM0008943         BM0008943         BM0008943         BM0008943         BM0008943         BM00008943         BM00008943         BM00008943         BM00008943         BM00008943         BM00008943         BM00008943         BM00008943         BM000008943         BM000008943         BM000008943         BM000008943         BM000008943         BM000008943         BM0000008943         BM000000999         BM00000099         BM00000099         BM00000099         BM00000099         BM00000099         BM00000099         BM000000099         BM00000009         BM00000009         BM00000009         BM00000009         BM00000009         BM00000009         BM00000009         BM000000009         BM000000000         BM000000000         BM0000000000         BM0000000000         BM0000000000         BM00000000000         BM0000000000         BM0000000000000         BM000000000000         BM0000000000000         BM000000000000         BM000000000000         BM0000000000000         BM0000000000000         BM00000000000000         BM0000000000000         BM000000000000000         BM000000000000000         BM00000000000000000000000         BM00000000000000000000000         BM000000000000000000000000000000000000	4         938         38.2         735         12         BM008943         BM008943         BM008943           5         93.5         38.0         2081         11         AK079650         AK079650         AK079650         AK079650         AK079650         AK079650         AK079650         AK079650         BK064739         BK064739         BK064739         BK064739         BK064739         BK064739         BK064739         BK064739         BK125038         BK125038         BK125038         BK125038         BK125039         BK140667         BK140667         BK140667         BK140667         CKB125031         CKB1325312         CKB1322312         CKB1322312<	33	47.	٠.	m	12	758	17581 60306594
5 933.5 38.0 2081 11 AK079650 AK079650 AK079650 O 33.5 38.0 2081 11 AK079650 AK079650 AK079650 O 33.3 37.9 994 13 BQ644799 BY56238 BY5623312 GY327128 GY3674156 BY674156 GY327128 GY34156 GY374156 GY3741	5         93.5.         38.0         2081         11         AK079650         AK079650         AK079650           6         93.1         37.1         683         13         BQ644799         BQ644739         BQ644739         BQ644739         BQ644739         BQ644739         BQ644739         BQ644739         BQ6742439         BQ6742439         BQ67437128         BQ67437128         BQ67437128         BQ67437128         BQ67437128         BQ67437128         BQ6744156         BQ6744156         BQ6744156         BQ6744156         BQ6744156         BQ6744156         BQ6744156         BQ744156         BQ741	34	93	œ,	73	12	894	18943 60361874
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7 912.5 37.1 683 13 BY750238 BY750238 BY750238 B 8750238 B 8750238 B 8672439 B 86812439 B 8672439 B 86812439 B 86812439 B 8672439 B 888.5 36.2 908 14 CA227128 CA327128 CA32712 CA327128 CA32712 CA32712 CA32712 CA32712 CA327312 CA3727312 CA3727412 CA37412 C	7 912.5 37.1 683 13 BY550238 BY550233 BY550233 BY550233 BY550233 BY550233 BY550233 BY550233 BY55023 BY5502 BY5502 BY5502 BY5502 BY5502 BY55	36	93	۲.	$\omega$	13	479	1799
8         900         36.6         638         10         BB612439         BB612432         BB612439         BB612432         BB612432         BB612432         BB612432         BB612432         BB612436	8         900         36.6         638         10         BB612439         BB6124156         BB6124156         BB6124156         BB6124156         BB6124156         BB614156	37	12.	,	m	13	023	0238
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0 888.5 36.2 908 14 CA227128 CA227128 U 870 35.4 97 13 BQ944156 BQ944156 BQ944156 BQ944156 BQ944156 J 869 35.4 974 12 B1402088 B1402088 B1402088 B1402088 B17.5 34.1 510 B1740667 CB586069 CB586069 CA32312 CA	0 888.5 36.2 908 14 CA.27128 CA.27128 U 870 35.4 974 13 BQ944156 BQ944156 BG944156 B1402088 B1402088 B1402088 BF1402088 BF140667 839 34.1 917 10 BF140667 CBS66069 CBS66069 CBS66069 GB37.5 34.0 647 14 CA.322312 CA.322312 CA.322312 CA.322312 CA.322312 CA.322313 CBS66069 FB140667 CBS66069 FB140667 CBS66069 FB14067	39	88	v.	$\circ$	10	07921	3217 F
1 870 35.4 974 13 BQ944156 BQ944156 Z 2 869 35.4 594 12 BI402088 BI402088 BI402088 N 3 839 34.1 917 10 BI410067 BF140667 BF140667 G 4 837.5 34.1 584 14 CB586069 CB586069 Z 5 834.5 34.0 647 14 CA322312 CA322312	1 870 35.4 974 13 BQ944156 BQ944156 Z 869 35.4 594 12 BI402088 BI402088 BI402088 B 3 839 34.1 917 10 BF140667 Z 4 837.5 34.1 584 14 CA322312 CA322312 CA322312 CA322312	40	88.	'n		14	A32712	7128 U
2 869 35.4 594 12 BI402088 BI402088 N 3 839 34.1 917 10 BF140667 BF140667 CB586069 CB586069 CB586069 CA322312 CA322312	2 869 35.4 594 12 BI402088 BI402088 N 3 839 34.1 917 10 BF140667 BF140667 E 4 837.5 34.1 584 14 CB586069 CB586069 F 5 834.5 34.0 647 14 CA322312 CA322312 CA322312 C	41	~	'n	~	13	94415	1156 7
3 839 34.1 917 10 BF140667 BF140667 60178691 4 837.5 34.1 584 14 CBS66069 CBS66069 AMGNUCC. 8 834.5 34.0 647 14 CA322312 CA322312 UI-M.FXO	3 839 34.1 917 10 BF140667 BF140667 6017 4 837.5 34.1 584 14 CB586069 CB586069 AMCN 5 834.5 34.0 647 14 CA322312 CL-M	42	1n	·	4	12	40208	2088 N
4 837.5 34.1 584 14 CB586069 CB586069 AMGNNUC: 5 834.5 34.0 647 14 CA322312 CA322312 UI-M-FX0	4 837.5 34.1 584 14 CB586069 CB586069 AMGNN 5 834.5 34.0 647 14 CA322312 CA322312 UI-M-	43	83	_;		10	14066	1698/109 /990
5 834.5 34.0 647 14 CA322312 CA322312 UI-M-FX	5 834.5 34.0 647 14 CA322312 CL-M-	44	37.		m	14	58606	5069 AMGNNUC:
		45	34.			14	32231	312 UI-M-FX

## ALIGNMENTS

RESULT 1 AK081806 LOCUS DEFINITION

AK081806

2101 bp mRNA linear HTC 20-SEP-2003
Mus musculus 16 days embryo head cDNA, RIKEN full-length enriched
library, clone:Cl30078K14 product:solute carrier family 2,
(facilitated glucose transporter), member 8, full insert sequence. AKO81806.1 GI:26349396
HTC; CAP trapper.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinse; AK081806

ORGANISM

ACCESSION VERSION KEYWORDS SOURCE

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/LTATES ALLONG TO THE TOTAL TO THE TOTAL TO THE TOTAL TOTAL TO THE TOTAL TOTAL
                                                                                                               /tissue_type="head"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  141 AlabrovalTyrIleSerGluIleAlaTyrProAlaValArgGlyLeuLeuGlySerCys 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ValGlnLeuMetValValValGlyIleLeuLeuAlaTyrLeuAlaGlyTrpValLeuGlu 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MetThrProGluAspProGluGluThrGlnProLeuLeuGlyProProGlyGlySerAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 ATGTCTCCCGAGGACCCCCAGGAGACGCAGCGCTATTGCGGCCACCGGAAGCCAGGACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 CCCGCGCGCCGCCGCCGTCCTTCCTTCGTCCCCCCCTCTGGGACCCCTCAGCTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AlaAlaGlyGlyValLeuGlyGlyTrpLeuValAspArgAlaGlyArgLysLeuSerLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCTGCAGGGGCATACTGGGCGGCTGGCTCCTGGACCGTGCAGGCGCAAGCTGAGCCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Trácticracaccaraccerricaraacracerriracrarcaccacaacacagarara
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCACCGGTTTACATCTCGGAAATCGCCTACCCAGCTGTCCGAGGACTGCTCGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21 ProArgGlyArgArgValPheLeuAlaAlaPheAlaAlaAlaLeuGlyProLeuSerPhe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 AlaProArgLeuAspAspAlaAlaAlaSerTrpPheGlyAlaValValThrLeuGlyAla
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                                                                                                                                                                                                                                                                                  /note="unnamed protein product; putative solute carrier family 2, (facilitated glucose transporter), member 8 (MOD|MGI:1860103, GB|NM_019488, evidence: BLASTN, 99%, match=1490)"
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61. .1494
                                                                                                                                                                                                                                                                                                                                                                                                                                                 /codon_start=1
/protein_id="BAC38338_1"
/db_xref="G1:26349397"
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                                                                             'clone="C130078K14"
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)

E (bases 1 to 2101)

E (bases 1 to 2101)

E Adachi, J., Aizawa, K., Akimura, T., Hara, A., Hashizume, W., Hayashida, S., Furuno, M., Hangaxi, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Katoh, H., Kawai, J., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saitoh, H., Sakai, C., Sakai, K., Saitoh, H., Sakai, C., Sakai, K., Shinagawa, A., Shiraki, T., Sagaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sagaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M., and Hayashizaki, Y., Poircet, Submission, M., Sasion, M., Sasion, M., Sasion, M., Tagawa, A., Tayanshi, F., Takaku-Akahira, S., Direct, Submission, M., Sasion, M., Tagawa, A., Toya, T., Yasunishi, A., Direct, Submission, M., Sasion, M., Sasion, M., Sasion, M., Sasion, M., Sasion, M., Sasion, M., Tagawa, A., Tayanishi, A., Tayahira, S., Tagami, M., Tagawa, A., Toya, T., Yasunishi, A., Direct, Submission, M., Sasion, S., Tagami, M., Tagawa, A., Toya, T., Yasunishi, A., Direct, Submission, M., Sasion, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Suni, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Mateumoto, R., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yonacaki, Y., Bhikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer 20530913
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RIKEN Genome Exploration Research Group Phase II Team and the
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The FANTOM Consortium and the RIKEN Genome Exploration Research
                                                                                                                                                                                                                                                                                  Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new Genome Res. 10 (10), 1617-1630 (2000)
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Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)
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Please visit our web site for further details.
URL:http://ganome.gc.riken.go.jp/
URL:http://fantom.gsc.riken.go.jp/.
Location/Qualifiers
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                                      Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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/mol_type="mRNA"
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Zhang, P.P., Zhou, X.M., Jiang, H.Q., Hu Wan, D.F. and Gu, J.R.
Direct Submission
Submitted (17-JUL-2000) National Labo Genes, Shanghai Cancer Institute, 25/20032, P. R. China
Location/Qualifiers
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    /organism="Homo sapie:
/mol_type="mRNA"
    /db_xref="taxon:9606"

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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                              ValileGlnValLeuPheThrAlaValAlaAlaLeuIleMetAspArgAlaGlyArgArg
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LSGVVMVFSTSAFFRLTNGGGPGNSSHVMISAPVSAQPVDASVGLAWLAVGSMCLF
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1 (bases 1 to 1954)
Zhang,P.P., Zhou,X.M., Jiang,H.Q., Huang,Y., Qin,W.X.,
Wan,D.F. and Gu,U.X.
Novel human cDNA clones with function of inhibiting can
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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ORGANISM Homo sapiens  Bikaryota; Merazoa; Chordata; Craniata; Vertebrata; Buteleostomi;  REFERENCE   Chaeses 1 to 1008   AUTHORS   Clark, A.G., Glanowski.S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Perriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.  TITLE   Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios   G552), 1960-1963 (2003)   PUBMED   4671902   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., PUBMED   4671902   AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Ferriera,S., Wang,G., Lanowski,S., Nielson,R., Sninsky,J.J., Ferriera,S., Wang,G., Lanowski,S., Nielson,R., Sninsky,J.J., Ferriera,S., Wang,G., USA   Course on alignment   Cookers of the based on alignment   Cookers o	ignment Scores:  ed. No.:  1713.00 Matches: 332 ove: 1713.00 Matches: 332 rocarl Similarity: 99.10\$ Mismatches: 29 Gaps: 0 -09-886-954A-1 (1-477) x AY414180 (1-1008)  143 ValTyrlleSerGluIleAlaTyrProAlaValArgGlyLeuLeuGlySerCysValGln	Db   1 GTCTACATCTCCGAAATCCCTACCTACTCCGGGGGTTGCTCGGTCTCGTTGTGTGCAG	Oy 243 PheHisLeuAlaLeuArgGlnProGlyIleTyrLysProPheIleIleGlyValSer 262
160 481 180 200 601 661 721 721 721 721 721 901	320 uLeuLeuValLeuSerGlyValValMetValPheSerThrSerAlaPheGlyAlaTyrPh 961 GCTCCTGGTCTTGTCAGGTCATGGTCATCAGCACGAGTCCCTTCGGCGCTACTT 340 eLysLeuThrGlnGlyGlyProGlyAsnSerSerHisValAlaIleSerAlaProValSe	11	Db 1234 CTGAAACTAAAGGAAAGACTCTGGAACAATCACAGCCCATTTTGAGGGGCGA 1286 RESULT 3 AY414180 LOCUS AY414180 DEPINITION Homo sapiens SLC2A8 gene, VIRTUAL TRANSCRIPT, partial sequence, ACCESSION AY414180. AY414180. AY414180. AY414180. GSS. SOURCE Homo sapiens (human)

/note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."	Alignment Scores: 9.65e-125 Length: 1201 Pred. No.: 1490.50 Matches: 320 Percent Similarity: 68.72\$ Conservative: 3 Best Local Similarity: 68.09\$ Mismatches: 23 Query Match: 127 DB: 127	l) InProLeuLeuGlvPro		21 FroArgG.LyArgWalFneLeuAlaAlaFneAlaAlaAlaLeuG.LyFroLeUSeFrNe 138	1 dryrichtabeudrylitserserrichtoralierroserbeuglichtghlantarrorio 6	ol Alakroargueuaspaspalaalaaserirpkneulyalavalvalinrueudyala	81 AlaAlaGlyGlyValLeuGlyGlyTrpLeuValAspArgAlaGlyArgLysLeuSerLeu 10	Oy 101 LeuLeuCysSerValProPheValAlaGlyPheAlaValI1eThrAlaAlaGlnAspVal 120  Db 138	Db   138 138   Cy   141 AlaProValTyrIleSerGluIleAlaTyrProAlaValArgGlyLeuLeuGlySerCys 160   Ch   139   Confirm Date of the confirmation of	161 ValGlnLeuMetValValValGlyIleLeuLeuAlaTyrLeuAlaGlyTrpValLeuGlu	Oy 181 TrpArgTrpLeuAlaValLeuGlyCysValProProSerLeuMetLeuLeuMetCys 200	312 THAIGCCGAGACCCGGCTTCCTGCTCAGCTCAGCGCCCAGGGGCCTCTCTTCTTCTGCTCAGCTCAGCGCCCAGGGGCCAGGGCCAGGGCCAGGGCCAGGGCCAGGGCCAGGGCCAGGGCCAGGGCCAGGGCCAGGGCCAGGGCCAGGGCCAGGGCCAGGGCCAGGGCCAGGGCCAGGGCCAGGGCAGGCCAGGGCCCCCC	OY 241 GINSERTRALELELEGIZGINFICOLYLISTINGSTROELELIEGIY 260  Db 432 CAGAGCTTTCACCTGGCCCTGCTGCGCACCTCTACAAGCTCTTHATCATCGGC 491  OY 261 ValSerLeumetAlaPheGlnGlnLeuSerGlyValAsnalaValMetPheTyralaGlu 280
Oy 303 ValLeuPheThrAlaValAlaAlaLeuIleMetAspArgAlaGlyArgArgLeuLeuLeu 	323 ValLeuserGlyValValMetValPheserThrSerAlaPheGlyAlaTyrPheLysLeu 3  [	Oy 363 ProValAspAlaSerValGlyLeuAlaTrpLeuAlaValGlySerMetCysLeuPheIle 382	Qy 383 AlaGlyPheAlaValGlyTrpGlyProIleProTrpLeuLeuMetSerGluilePhePro 402	Qy 403 LeuHisValLysGlyValAlaThrGlyIleCysValLeuThrAsnTrpLeuMetAlaPhe 422	Oy 423 LeuValThrLysGluPheSerSerLeuMetGluValLeuArgProTyrGlyAlaPheTrp 442	Oy 443 LeuAlaSerAlaPheCysIlePheSerValLeuPheThrLeuPheCysValProGluThr 462	Qy 463 LysglyLysThrLeuGluGlnIleThralaHisPheGluGlyArg 477	RESULT 4  BX395379  LOCUS  BX395379  BX395379  LOCUS  DEFINITION  BX395379  Homo sapiens  BENINITION  BX395379  Homo sapiens  BENINITION  BX395379  Homo sapiens	ACCESSION BX395379 VERSION BX395379.1 GI:30620615 KEYWORDS EST. SOURCE Homo sapiens (human) CORGANISM Homo sapiens		AL Unpublished (2001) Context: Genoscope Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - France BRail: seqref@qenoscope.cns.fr, Web: www.genoscope.cns.fr Library was Constructed by Life Rechardonies a division	1 CO	FEATURES  Location/Qualifiers  11201  /organism="Homosapiens"  //organism="Homosapiens"  /do xref="teaxon:9606"  /clone="CSODDO06XP06"  /tissue type="NEUROBLASTOMA COT 50-NORMALIZED"  /clone_lib="Homo sapiens NEUROBLASTOMA COT 50-NORMALIZED"

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61 CTGATGSTTGTCACTGGCATCCTCGGCCTATGTGGCAGGCTGGGTCCTAGAGTGGCGC
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Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 1000)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
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(lark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Perriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering
them based on alignment.
                                                                                                                                                                                                                                                                                                  PhelleAlaGlyPheAlaValGlyTrpGlyProlleProTrpLeuLeuMetSerGlulle
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                                                                                                         LeuLeuValleuSerGlyValValMetValPheSerThrSerAlaPheGlyAlaTyrPhe
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BG479842 932 bp mRNA linear EST 21-MAR-2001 602527373F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:4650906 5',
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/clone="InAce:"F126945"
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/lone lib="NHIDB"
/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: ECORV
/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: br
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 1085)
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Email: cgapbe-r@mail.nh.gov
Tissue Procurement: Invitrogen
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
Plate: LLAM12720 row: d column: 18
High quality sequence stop: 679.
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NIH-MGC http://mgc.nci.nih.gov/.
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BG700749 830 bp mRNA linear EST 07-MAY-2001
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Final: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://ange.lln.gov
Plate: LLAMN10709 row: p column: 04
High quality sequence stop: 789.
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11 HOMG http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
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                                                                                                                                                                                                                                                    542 GGGCTGGGAAGACCCCCCCATCGGGGCTGAGCAGAGCTTTCACCTGGCCCTGCTGCGGCA
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                                                 ThrGlnHisArgArgGlnGluAlaMetAlaAlaLeuArgPheLeuTrpGlySer-GluGl
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/note="Organ: brain; Vector: pBluescriptR (modified Pabluescript KS+); Site_1: BamHI, Site_2: SalI-XhoI (grogag); Oligo-dI primed using primer
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mol_type="mRNA"
/db xref="taxon:9606"
/clone="IMAGE:4814451"
/tissue_type="hippocampus"
/lab host="DH10B"
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Site 2: EcoRI; cDNA made by oligo-dT priming.

Directionally cloned into BcoRI/AhOI sites using the following 5' adaptor: GGGACGAG(G). Size-selected >500pp for average insert size 1.8kb. Library constructed by ing Hong in the laboratory of Gerald M. Rubin (University of Galifornia, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
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   National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                               Email: crapbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can lfound through the I.M.A.G.E. Consortium/LLNL at:
Plate: LLCMA433 row: a column: 19
High quality sequence stop: 820.
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/tisene type="choriocarcinoma"
/lab host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_21"
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                                                                      Contact: Robert Strausberg, Ph.D.
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/db_xref="taxon:9606"
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/db_xref="taxon:9606"
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5'-TTTTTTTTTTTTTTTVN-3', size-selected for average insert size 2.5 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIMH/NHGMI, National Institutes of Health). Note: this is a NIH_MGC Library."
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991 bp mRNA linear EST 30-JUL-2001 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:5141007 5',
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/clone lib="NUH MGC 12"
/note="Organ: cervix; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.4 kb. Library prepared by Life
Technologies."
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                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleosto
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Bases 1 to 991)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                     Email: complement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Incyte Genomics, Inc.
CDNA Library Arrayed by: Incyte Genomics, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov f. column: 16
High quality sequence stop: 835.
Location/Qualifiers
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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RESULT 10  AV414181 LOCUS DEFINITION Pan trogolodytes SLC2A8 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.  ACCESSION VERSTON AV414181. VERSTON AV414181. VERSTON GSS 17-DEC-2003 AV414181. GI:39770143 AV414181 AV414181 GI:39770143 AVA14181 AV414181 GI:39770143 AVA14181 GI:39770143 AVA14181 AVA14181 AV414181 GI:39770143 AVA14181		source 1l004 /organism="Pan troglodytes" /mol type="genomic DNA" /db_xref="taxon:9598" /db_xref="taxon:9598" /locus_tag="HCM5138"	ment Scores: No.: 1.04e-104 1269.00 it Similarity: 79.88% Local Similarity: 78.98% Match: 51.65%	US-09-886-954A-1 (1-477) x AY414181 (1-1004)  Qy	Db 63 GTCGTCGTCGTCGTCGTCGTCTACTGGCANNNNNNNNNNN	Qy 205 ThrProArgPheLeuLeuThrGlnHisArgArgGlnGluAlaMetAlaalaLeuArgPhe 224  Db 183 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
09 101 LeuLeuCysSerValProPheValAlaGlyPheAlaValIleThrAlaAlaGlnAspVal 120 72	GCGCCCCCCCCCTCATGCTGCTTCTCATG   GCGTGCCCCCCCCCTCATGCTGCTTCTCATG   GCGTGACGCTGCTGCTTCTCATG   GCGTGACTGCTGCTGTTGTTTTTTTTTTTTTTTTTTTTT	261 ValSerLeuMetAlaPheGlnGlnLeuSerGlyValAsnalaValMetPheTyralaGlu 280	IleGInValLeuPheThralaValAlaAlaLeuIleMetAspArgAlaGlyArgArgLeu 	341 Lysteuthridinglydrydrodryanserser-Hisvalatalieseralarvodryalse 360  667 Aagctgacccagggaggccctgggaacrccrcgcaacgrogccarcrcggcgcccrgrcrc 726  360 ralagin-Provalaspalaserval-GlybeualatrpLeualaval-Glyserwercy 379	379 sLeupheileAladlyPheAlaValGlyTrpGlyProlleProTrpLeuLeuMe 397	847 TCAGARGATCTTTCCCCTCTGCATTGTCAGGGGCGTGGGGGCATT 897 412 eCysValleuThrAshTrpLeuMetalaPheLeuValThrLysGluPheSerSerLeuMe 432 412 eCysValleuThrAshTrpLeuMetalaPheLeuValThrLysGluPheSerSerLeuMe 432 898 CTAGGTCCCACAAATGGCTCCATGGCCTTTCCGGGACCAG-GAGTTCAGCCAGCTCTT 956 432 tGluValLeuArgProTyrGlyalaPheTrpLeuAla 444 132 tGluValLeuArgProTyrGlyalaPheTrpLeuAla 444 141

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303 CTGGCCCTGCTGCGCCAGCCCGGCATCTACAAGCCCTTCGTCATCGGCGTCTCCCTGATG 362
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
                                                                  363 GCCTTCCAGCAGCTGCGGGGGTCAACGCCGTCATGTTCTATGCAGAGACCATCTTTGAA
                                                                                                                                GluAlaLysPheLysAspSerSerLeuAlaSerValValValGlyValIleGlnValLeu
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                                           265 AlaPheGinGinLeuSerGlyValAsnAlaValMetPheTyrAlaGluThrilePheGlu
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Bldg. 31 Rm10A07 Bethesda, MD 20892
Bmail: cgapbs-remail.ih.gov
CDNA Library Preparation: Invitrogen Corp
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can I found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CD557801

875 bp mRNA linear ES:
AGENCOURT 14413291 NIH MGC 180 Homo sapiens cDNA clone
IMAGE:30386912 5', mRNA sequence.
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/lab host="NHH_MGC_40"
/clone_lib="NHH_MGC_40"
/note="Torgan: prostate; Vector: porB7; Site_1: Xho1;
Site_2: BcoR1; conNA made by oligo-dT priming.
Directionally cloned into BcoR1/Xho1 sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kylon (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                            603621486F1 NIH_MGC_40 Homo sapiens cDNA clone IMAGE:5447181 5', mRNA sequence.
E | (Dases | to 880)

NIH-MGC http://mgc.nci.nh.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nh.gov
Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Preparation: Ling Hong/Rubin Laboration
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1930 row: k column: 22
http://image.llnl.gov
Plate: LLCM1930 row: k column: 22
High quality sequence stop: 869.

1. .880
Corganism="Homo sapiens"
//doganism="Homo sapiens"
//dofanism="Homo sapiens"
//dome="HRAGE:5447181"
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//lish homet="HRAGE:5447181"
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 880)
                                                                          316 AlaGlyArgArgLeuLeuLeu-ValLeuSerGlyVal-ValMet-ValPheSerThrSer
                                                                                                                                                                         Ala--PheGlyAlaTyrPheLysLeu--ThrGlnGlyGlyProGlyAsnSerSer 351
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602522606F1 NIH_MGC_20 Homo sapiens CDNA clone IMAGE:4641145 5',
mRNA sequence.
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                                                                                                                                                          uAlaSerAlaPheCysIlePheSerValLeuPheThrLeuPheCys-ValProGluThrL 463
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/clone lib="NIH MGC_20"

ECRI; CDNA made by Oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following s' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 828)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ArC/DCTD/DTP
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lln.gov
Plate: LLCMI407 row: & column: 02
High quality sequence stop: 788.
576 CGCCTTTGCGGTGGGCTGGGGCCCATCCCCTGGCTCCTCATGTCAGAGATCTTCCCTCT
                                                                                                                                                                              423 uValThrLysGluPheSerSerLeuMetGluValLeuArgProTyrGlyAlaPheTrpLe

      uHisValLysGlyValAlaThrGlyIleCysValLeuThrAsnTrpLeuWetAlaPheLe

                                                            636 GCATGTCAAGGGCGTGGCGACAGGCATCTGCGTCCTCACCAACTGGCTCATGGCCTTTCT
                                                                                                               696 CGTGACCAAGGAGTTCAGCAGCCTCATGGAGGTCCTCAGGCCCTATGGAGCCTTCTGGCT
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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/mol_type="mRNA"
/mol_tref="taxon:9606"
/clone="INAGE:4641145"
/tissue_type="melanotic melanoma"
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BG717034 1777 bp mRNA linear EST 08-MAY-2001 602689093F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:4821598 5',
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                         167 GECTTCGCGCTCGGCTACAGCTCCCCGGCCATCCCTAGCCTGCAGCGCGCCCCCGG
                                           47 ATGACGCCCGAGGACCCAGAGGAAACCCAGCGCTTCTGGGGGCTCCTGGCGGCAGCGCG
                                                                                                                                                                                                                                                                                                                                                               227 GCCCGGGCCTGCACAAGCCGCGCCTCCTGGTTCGGGGCTGTCGTGAACCCTGGGTGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               347 TIGCTGTGCTCCGTGCCCTTCGTGGCCGGCTTTGCCGTCATCACCGCGGCCCAGGACGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      767 GAGCAGAGCTITCACCTITGGCCCTTGITGCGGAAGCCCGGCATCTACAAGCCCTTCATCA
                                                                                                                                                               107 CCCCGCGGCGCCGCGCTTCCTCGCCGCCTTCGCCGCTGCCCTGGGCCCACTCAGCTTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 527 GTGCAGCTAATGGTCGTCGTCGGCATCCTTCTTGGCCTTACCTGGCAGGCTGGGTGCTGG
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MetThrProGluAspProGluGluThrGlnProLeuLeuGlyProProGlyGlySerAla
                                                                                                                                                                                                                    GlyPheAlaLeuGlyTyrSerSerProAlaIleProSerLeuGlnArgAlaAlaProPro
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NIH-MCC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BG717034.1 GI:13996221
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BG717034
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200 635 695 240

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/clone="Organ: Drain; Vector: pCMV-SPORT6; Site_1: NotI;

/note="Organ: Drain; Vector: pCMV-SPORT6; Site_1: Note: pCMV-SPORT6; Not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               603029344F1 NIH_MGC_114 Homo sapiens cDNA clone IMAGE:5199778 5', mRNA sequence.
                                                                                                                                                                                                                            PheMetProGluThrProArgPheLeuLeuThrGlnHisArgArgGlnGluAlaMetAla 220
                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 889)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conteact: Robert Strausberg, Ph.D.

Conteact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
   Tissue Profurement: Life Technologies, Inc.
   CDNA Library Preparation: Life Technologies, Inc.
   CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
   DNA Sequencing by: Incyte Genomics, Inc.
   Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/Link at:
   http://image.llnl.gov
   Plate: LiAM11500 row: g column: 11
   High quality sequence stop: 877.
   Location/Qualifiers

rce
                          ValGlnLeuMetValValGlyIleLeuLeuAlaTyrLeuAlaGlyTrpValLeuGlu
                                                    TrpArgTrpLeuAlaValLeuGlyCysValProProSerLeuMetLeuLeuLeuMetCys
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TITLE
JOURNAL
COMMENT
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LOCUS
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/clone lib="NITH MGC 97"
/clone fiorgan: testis; Vector: pBluescriptk (modified pBluescriptk K8+1) Site_1: BamHI; Site_2: Sall-XhoI (gtcgag); Oligo-dT primed using primer
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                                                                            Shiraki
               Enail: cgapber:enail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shirak
CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shirak
Toshiyuki and Piero Carninci (RIREN)
DNA Sequencing Dy: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/Link at:
http://image.llni.gov
Plate: LiAMI0728 row: i column: 23
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  Contact: Robert Strausberg, Ph.D.
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ago ,	38 GICTACATCICCGAAAICGCCTACCCAGCAGTCGGGGGGTTGCTCGGCTCCTGTGTGCAG 97
충 웜	163 LeuMetValValValGly11eLeuLeuAlaTyrLeuAlaGLyTrpValLeuGluTrpArg 182 98 CTAATGGTGGTGGTGGGARCCTCCTGGCTACCTGGCA136
λō	3 TrpLeuAlaValLeuGlyCysValProProSerLeuMetLeuLeuLeuMetCysPheMet 20
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δλ	ArgPheLeuTrpGlySerGluGlnGlyTrpGluAspProProlleGlyAlaGluGlnSer 2.
qq	137GAG 139
8	243 -PheHisLeuAlaLeuArgGlnProGlylleTyrLysProPhelleIleGlyValSe 262
QQ	CTIGGCCCTIGTIGGGCCGGCATCTACAAGCCCTTCATCATCGGCGTCTC
δλ	62 rLeuMetAlaPheGlnGlnLeuSerGlyValAsnAlaValMetPheTyrAlaGluThr11 28;
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8 8	282 ePheGluGluAlarysPheLysAspSerSerLeuAlaSerValValValGlyValIleGl 302
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δλ	22 uValLeuSerGlyValValMetValPheSerThrSerAlaPheGlyAlaTyrPheLysLe 34
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δy	342 uThrGlnGlyGlyProGlyAsnSerSerHisValAlaIleSerAlaProValSerAlaGl 362
q <sub>O</sub>	A-GGTGGCCCTGGCAACTCCTCGCACGTGGCCATCTCGGCGCCTGTCTCTGCACA 49
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٥'n	382 eAlaGlyPheAlaValGlyTrpGlyProIleProTrpLeuLeuWetSerGluIlePhePr 402
qq	Gecedentingedestradedeceancecraectecterandreagaaten
72	402 oLeuHisValLysGlyvalAlaThrGlyIleCysValLeuThrAsnTrpLeuMetAlaPh 422
qq	619 TCTGCATGTCAAGGGGGTGGCGACAGGCATCTGCGTCCTCACCAACTGGCTCATGGCCTT 678
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Ωρ	:TCCGTTTCTGATCTTCAGTGTCCTTTTCACTTTGTTCTGTGTCCCT
ر د د	462 rLysGlyLysThrLeuGluGlnIleThrAlaHisPheGluGlyArg 477 [1]
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Aba24791
Aba24791
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10-OCT-2001; 2001US-0328605P.
15-FEB-2002; 2002US-0357253P.
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOPEXT=7
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Aaf55865 Human GLU
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1 MTPEDPEETQPLLGPPGGSA......CVPETKGKTLEQITAHFEGR 477
        GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd
                                                     - nucleic search, using frame_plus_p2n model
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                                                                                                                                                                                                                                                    3373863 segs, 2124099041 residues
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Database :

Result М М us-09-886-954a-1.rng

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The present sequence is that of a human solute carrier type 2A (SLC2A)

nucleic acid Genetic screens were designed to identify modifiers of the
p33 pathway in Drosophila in which p53 was overexpressed. Human

orthologues (polynuclectides and polypeptides) of one such modifier were

then identified, including the present nucleic acid. SLC2As are glucose

transporter proteins with sugar transporter domains. SLC2A nucleic acids

and polypeptides are attractive drug targets for the treatment of

pathologies associated with a defective p53 signalling pathway, such as

cancer. The invention provides in vitro and in vivo methods of assessing

SLC2A function. Modulation of an SLC2A or its binding pathway as useful

cormal and disease conditions and for developing diagnostic and

therapeutic modalities of p53-related pathologies. SLC2A-modulating

agents that act by inhibiting or enhancing SLC2A expression, directly or

conditions and solved for as attransport or

binding activity, can be identified using methods provided. Modulators

conditions and conditions conditions conditions and conditions conditions 
                                                                                                                                                                                      Identifying candidate p53 pathway modulating agent as therapeutic target for disorders of defective p53 function e.g. cancer, by assaying purified solute carrier family 2 (SLC2A) polypeptide or nucleic acid with a test
RP;
Funke
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'n,
Francis-Lang
Belvin M,
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Plowman GD,
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Sequence 1445 BP; 182 A; 500 C; 456 G; 307 T; 0 U; 0 Other;

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                                                                                                              ProArgGlyArgValPheLeuAlaAlaPheAlaAlaAlaLeuGlyProLeuSerPhe
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Conservative:
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(first entry)

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Human; solute carrier type 2A; SLC2A; glucose transporter; p53; cancer; cytostatic; gene therapy; gene; ss.
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                                                                                                                                                  Belvin M, Francis-Lang H,
      Human solute carrier type 2A nucleic acid 13642003.
                                              Location/Qualifiers
4. .1437
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                                                                                                             05-JUN-2001; 2001US-0296076P.
10-OCT-2001; 2001US-0328605P.
15-FEB-2002; 2002US-0357253P.
                                                                                                  03-JUN-2002; 2002WO-US017419.
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                                                                                                                                     (EXEL-) EXELIXIS INC.
                                                                                                                                                            WPI; 2003-201283/19.
P-PSDB; ABP58364.
                                                                          WO200298467-A1
                                  Homo sapiens
                                                                                       12-DEC-2002
                                                                                                                                                 Friedman L,
                                              Key
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Identifying candidate p53 pathway modulating agent as therapeutic target for disorders of defective p53 function e.g. cancer, by assaying purified solute carrier family 2 (SLC2A) polypeptide or nucleic acid with a test agent

Disclosure; Page 42-43; 58pp; English.

The present sequence is that of human solute carrier type 2A (SLC2A)

nucleic acids 13642003. Genetic screens were designed to identify

modifiers of the p53 pathway in Drosophila in which p53 was

coverexpressed. Human orthologues (polynucleotides and polypeptides) of

one such modifier were then identified, including nucleic acid 13642003.

SLC2As are glucose transporter proteins with sugar transporter domains.

SLC2A nucleic acids and polypeptides are attractive drug targets for the

treatment of pathologies associated with a defective p53 signalling

pathway, such as cancer. The invention provides in vitro and in vivo

methods of assessing SLC2A function. Modulation of an SLC2A or its

binding partners is useful for understanding the association of the p53

pathway and its members in normal and disease conditions and for

developing diagnostic and therapeutic modalities of p53-related

bathologies. SLC2A-modulating agents that act by inhibiting or enhancing

SLC2A expression, directly or indirectly, e.g. by affecting an SLC2A

function such as transport or binding activity, can be identified using

methods provided. Modulators include small molecules, nucleic acids,

antibodies, antisense oligonucleotides and phosphothioate morpholino (claimed) oligomers

Sequence 1856 BP; 262 A; 624 C; 573 G; 397 T; 0 U; 0 Other;

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	1.42e-204	2457.00	100.00%	100.00%	100.00%	7
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US-09-886-954A-1 (1-477) x ABZ24792 (1-1856)

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1 MetThrProGluAspProGluGluThrGlnProLeuLeuGlyProProGlyGlySerAla 20	4 ATGACGCCCGAGGACCCAGAGGAAACCCAGCCGCTTCTGGGGCCTCCTGGCGGCAGCAGC

<i>\$</i> 65	21	21 ProArgGlyArgArgValPheLeuAlaAlaPheAlaAlaAlaLeuGlyProLeuSerPhe 40 [
Qy	41	GlyPheAlaLeuGlyTyrSerSerProAlalleProSerLeuGlnArgAlaAlaProPro 60
QQ	124	
λŏ	61	AlaProArgLeuAspAspAlaAlaAlaSerTrpPheGJyAlaValValThrLeuGJyAla 80
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٥¾	81	AlaAlaGlyGlyValLeuGlyGlyTrpLeuValAspArgAlaGlyArglysLeuSerLeu 100
Op	244	GCGGCGGGGGGAGTGCTGGGCTGGTGGACCGCGCCGGGCGCGAGCTGAGCTC 303
δλ	101	LeuLeuCysSerValProPheValAlaGlyPheAlaValIleThrAlaAlaGlnAspVal 120
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ò	121	TrpMetLeuLeuGlyGlyArgLeuLeuThrGlyLeuAlaCysGlyValAlaSerLeuVal 140
Db	364	TGGATGCTGCTGGGGGGGCCGCCTCCTCACCGGCCTGGCGGTGTTGCTTGC
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QQ	424	GCCCGGGTCTACATCTCCGAAATCGCCTACCCAGCAGTCCGGGGGTTGCTCGGCTCCTGT 483
δ,	161	ValGInLeuMetValValValGlyIleLeuLeuAlaTyrLeuAlaGlyTrpValLeuGlu 180
Dβ	484	GTGCAGCTAATGGTCGTCGTCGTCGTCCTCCTGGCCTACCTGGCAGGCTGGGTGCTGGAG 543
٥٨	181	TrpArgTrpLeuAlaValLeuGlyCysValProProSerLeuMetLeuLeuMetCys 200
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٥y	221	AlaLeuArgPheLeuTrpGlySerGluGluGlyTrpGluAspProProlleGlyAlaGlu 240
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QY	241	GInSerPheHisLeuAlaLeuLeuArgGInProGlyIleTyrLysProPheIleIleGly 260
Dp	724	CAGAGCTITCACCTGGCCCTGCTGCGGCAGCCCGGCATCTACAAGCCCTTCATCAGGC 783
ογ	261	ValSerLeuWetAlaPheGlnGlnLeuSerGlyValAsnAlaValMetPheTyrAlaGlu 280
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δy	281	ThrilePheGluGluAlaLysPheLysAspSerSerLeuAlaSerValValValGlyVal 300
Db	844	ACCATCTTTGAAGAGGCCAAGTTCAAGGACAGCCTGGCCTCGGTCGTCGTCGTGGTC 903
δy	301	IleGlnValLeuPheThrAlaValAlaAlaLeuIleMetAspArgAlaGlyArgArgLeu 320
Db	904	ATCCAGGTGCTGTTCACAGCTGTGGCGGCTCTCATCATGACAGAGCAGGCGGAGGCTG 963
Οy	321	LeubeuValbeuSerGlyValValMetValPheSerThrSerAlaPheGlyAlaTyrPhe 340
qq	964	CTCCTGGTCTTGTCAGGTGTGGTCATCAGCACGAGTGCCTTCGGCGCCTACTTC 1023
Qy	341	LysteuThrGlnGlyGlyProGlyAsnSerSerHisValAlalleSerAlaProValSer 360
Dβ	1024	AAGCTGACCCAGGGTGGCCCTGGCAACTCCTCGCACGTGGCCATCTCGGCGCCTGTCTCT 1083
Qy	361	AlaGinProValAspAlaSerValGiyLeuAlaTrpLeuAlaValGiySerMetCysLeu 380
QQ	1084	GCACAGCCTGTTGATGCCAGCGTGGGCTGGCTGGCTGGGCTGGGCAGCATGTGCCTC 1143
Ογ	381	PhelleAlaGlyPheAlaValGlyTrpGlyProlleProTrpLeuLeuMetSerGlulle 400

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H, Nguyen DB, Yao MG, Gandhi
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Lal P, Hillman JL, Azimzai Y,
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The present sequence is transporter and ion channel-1 (TRICH-1) cDNA.

TRICH is used as vaccine. TRICH is useful for treating a disease or condition associated with decreased expression of functional TRICH, such as transport disorder including amyotrophic lateral sclerosis, cystic fibrosis, Becker's muscular dystrophy, angina and hypertension, neurological cuckers including Alzheimer's disease, ammesia, bipolar disease, disorders including Alzheimer's disease, ammesia, bipolar disease, cerebral neoplasms, Pick sdisease, Muntington's disease and parkinson's disease, demyelinating disease, mental disorders including extroped and seasonal affective disorders muscle mood, anxiety, Schizophrenia and seasonal affective disorders including deraction parkinson's disease, demyelinating diseases, mental disorders including AIDS, adult respiratory distress syndrome (ARDS), allergies, carantermyositis, arrhythmias and asthma and immunological disorders including AIDS, adult respiratory distress syndrome (ARDS), allergies, canaemia, diabetes mellitus, rheumatoid arthritis, scleroderma, Sjogren's syndrome, systemic lupus erythematosus and other diseases including sickle cell anaemia, Wilson's disease, cataracts, infertility, pulmonary sickle cell anaemia, Wilson's disease, disease, Addison's disease, contassis drave addisors, cancers confections. TRICH DNA is useful in gene therapy and in diagnostic
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preventing transport, neurological, muscle and immunological disorders
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The present sequence is that of human solute carrier type 2A (SLC2A) nucleic acids 7657680. Genetic screens were designed to identify mudifiers of the p53 pathway in Drosophila in which p53 was severable search the p53 pathway in Drosophila in which p53 was severable search modifier were then identified, including nucleic acid 7657680. SLC2As are glucose transporter proteins with sugar transporter domains. SLC2A nucleic acids and polypepides are attractive drug targets for the treatment of pathologies associated with a defective p53 signalling. Dathway, such as cancer. The invention provides in vitro and in vivo methods of assessing SLC2A function. Modulation of an SLC2A or its binding partners is useful for understanding the association of the p53 pathologies. SLC2A-modulating adents that act by inhibiting or enhancing SLC2A expression, directly or indirectly, e.g. by affecting an SLC2A function such as transport or binding activity, can be identified using methods provided. Modulators include small molecules, nucleic acids, antisense oligonucleotides and phosphothioate morpholino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Identifying candidate p53 pathway modulating agent as therapeutic target for disorders of defective p53 function e.g. cancer, by assaying purified solute carrier family 2 (SLC2A) polypeptide or nucleic acid with a test
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                                                   cocation/Qualifiers
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10-OCT-2001; 2001US-0328605P.
15-FEB-2002; 2002US-0357253P.
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Human; solute carrier type 2A; SLC2A; glucose transporter; p53; cancer;

Human solute carrier type 2A nucleic acid 7657680

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The present invention relates to GLUTX proteins (AAF55865-AAF55871 and AAB66931-AAB66941). The GLUTX proteins are related to the facultative glucose carriers GLUT1-GLUTS and have hexose binding and/or transport function. The GLUTX proteins may be used in the diagnosis, prevention and treatment of hexose transport discorders such as isothemia, diabetes, hyperglycaemia, hypoglycaemia, a glucose metabolism disorder and/or a neurodegenerative disease. The present sequence is the coding sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; GLUTX; gene therapy; vaccine; hexose transport modulator; hexose transport disorder; ischaemia; diabetes; hyperglycaemia; ss; hypoglycaemia; glucose metabolism disorder; neurodegenerative disease.
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2000US-00616132.
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1368 AAGCTGACCCAGGGTGGCCCTGGCAACTCCTCGCACGTGGCCATCTCGGCGCCTGTCTCT
                                                                                                                            GCACAGCCTGTTGATGCCAGCGTGGGCTGGCCTGGCCGTGGCCAACATGTGCCTC
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hexose transport disorder; ischaemia; diabetes; hyperglycaemia; ss;
hypoglycaemia; glucose metabolism disorder; neurodegenerative disease.
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                        479 T;
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                        580 G;
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Query Match:
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                                                                   GluThrilePheGluGluAlaLysPheLysAspSerSerLeuAlaSerValValGly
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                                              The present invention relates to GLUTX proteins (AAF55865-AAF55871 and AAB66932-AAB66941). The GLUTX proteins are related to the facultative glucose carriers GLUT1-GLUTS and have hexose binding and/or transport function. The GLUTX proteins may be used in the diagnosis, prevention at reatment of hexose transport disorders such as ischaemia, diabetes, hyperglycaemia, hypoglycaemia, a glucose metabolism disorder and/or a neurodegenerative disease. The present sequence is the coding sequence
                                                                                                                                                                                                                                                                                                                    MetThrProGluAspProGluGluThrGlnProLeuLeuGlyProProGlyGlySerAla
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protein with cancer suppressing function. The invention also comprises a method for preparing the polypeptide by recombination, and an application of the polypeptide in treating diseases such as cancer, etc. Also disclosed in an antagonist of the polypeptide and its medical action. The present sequence represents a CDNA encoding a cancer suppressing protein of the invention
                                                                                                                                                                                          This invention relates to the cDNA and protein sequences of a novel human
                                                                                  New human protein with cancer cell growth suppressing function and polynucleotide encoding it, for treating diseases, such as, cancer.
                                                                                                                                                5; Page 23-24 (disclosure); 39pp; Chinese.
                 WPI; 2002-609437/66.
P-PSDB; ABU11283.
                                                                                                                                                Claim
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CO TOO STEELS			
Pred. No.:	1.94e-175	Length:	1954
Score:	2123.50	Matches:	426
Percent Similarity:	89.14%	Conservative:	П
Best Local Similarity:	88.94%	Mismatches:	7
Query Match:	86.43%	Indels:	21
DB:	9	Gaps:	ч
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573 G; 423 T; 0 U; 0 Other;

BP; 325 A; 633 C;

Sequence 1954

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US-09-886-954A-1 (1-477) x ABX34029 (1-1954)

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QY	1 MetThrProGlu	uAspProGluGluThrGlnProLeuLeuGlyProProGlyGlySerAla 20
Db	1 GTGACGCCCGAG	GTGACGCCCGAGGACCCAGAGGAAACCCACGCCTTCTTGGGGCCTCCTGGCGCGAGCGCG 60
δλ	21 ProArgGlyArg	ProArgGlyArgArgValPheLeuAlaAlaPheAlaAlaAlaAlaLeuGlyProLeuSerPhe 40
Dþ	61 CCCCGCGGCCGC	CCCGCGCGCCGCGCGTTTTCCTCGCCGCTTTCTTCTTTTTT
οy	41 GlyPheAlaLeuGl	GlyTyrSerSerProAlalleProSerLeuGlnArgAlaAlaProPro 60
qa	121 GGCTTCGCGCTCGG	GGCTACAGCTCCCCGGCCATCCCTAGCCTGCGCGCGCGCG
δ	61 AlaProArgLeu	AlabroArgLeuAspAspAlaAlaSerTrpPheGlyAlaValValThrLeuGlyAla 80
Db	181 GCCCCGCGCCTG	GCCCGGGCCTGGAGGCGCCGCCGCCTCCTGGTTCGGGGCTGTCGTGAGCCTGGGTGCC 240
δλ	81 AlaAlaGlyGly	AlaAlaGlyGlyValLeuGlyGlyTrpLeuValAspArgAlaGlyArgLySLeuSerLeu 100
qq	241 GCGGCGGGGGG	GCGGCGGGGGGGGGTGGCTGGCTGGCTGGTGGTGGTGGTG
οy	101 LeuLeuCysSer	ervalproPheValAlaGlyPheAlaValIleThrAlaAlaGlnAspVal 120
qu	301 TIGCIGIGCIC	CGTGCCCTTCGTGGCCGGCTTTGCCGTCACCGCGGCCCAGGACGTG 360
δλ	121 TrpMetLeuLeu	TrpMetLeuLeuGlyGlyArgLeuLhrGlyLeuAlaCysGlyValAlaSerLeuVal 140
Db	361 TGGATGCTGCTC	HELLITIETTE TRANSPORTE
Qy	141 AlaProValTyr	TyrileSerGluileAlaTyrProAlaVal-ArgGlyLeuLeuGlySerCy 160
Db	421 GCCCCGGTCTAC	GCCCGGGTCTACATCTCCGAAATGGCCTACCCAGCAGTCCCGGGGGTTGCTCGGCTCCTG 480
٥x	160 sValGlnLeuMe	GlnLeuMetValValValGlyIleLeuLeuAlaTyrLeuAlaGlyTrpValLeuGl 180
Db	481 TGTGCAGCTAAT	GGTCGTCGTCGGCATCCTCCTGGCCTGCTGGCAGGCTGGCT
Š	180 uTrpArgTrpLe	uTrpArgTrpLeuAlaValLeuGlyCysValProProSerLeuMetLeuLeuMetCy 200
qq	541 GTGGCGCTGGCT	GIGGCGCTGGCTGGCTGGCTGCCTGCCTCCCTCCTCATGCTTCTTCATGT 600
δ	200 sPheMetProG	SPheMetProGluThrProArgPheLeuLeuThrGlnHisArgArgGlnGluAlaMetAl 220
Db	601 CTTCATGCCCG	CTTCATGCCCGAGACCCCGCGCTTCCTGCTGACTCAGCACAGGCGCCCAGGAGGCCCATGGC 660

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                                                                                      721 GCAGAGCITICACCIGGCCCIGCIGCGGCCAGCCCGGCAICTACAAGCCCTICATCGG
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                                                         uGlnSerPheHisLeuAlaLeuLeuArgGlnProGlyIleTyrLysProPheIleIleGl
                                                                                                                     yvalSerLeuMetAlaPheGlnGlnLeuSerGlyValAsnAlaValMetPheTyrAlaGl
                                                                                                                                                                             uThrilePheGluGluAlaLysPheLysAspSerSerLeuAlaSerValValValGlyVa
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                                                                                                                                                                                                                                            The invention relates to novel genes (ABL89449-ABL90853) and proteins (ABB89940-ABB90444) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital, (b) immune discretes e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) acatiowascular disorders such as myocardial ischaemias; (d) wound healing of the processing the sclerosis of the such as myocardial ischaemias.
                                                                                                                                                                                                                                                                                                                                                                                                     (e) neurological diseases e.g. cerebral anoxia and epilepsy, and (f) infectious diseases such as viral, bacterial, fungal and parasitic infections. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                      Novel 1405 isolated polypeptides, useful for diagnosis, treatment and prevention of neural, immune system, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal and proliferative disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BP; 177 A; 362 C; 345 G; 255 T; 0 U; 17 Other;
                                                                                                                                                                                                                   Claim 4; SEQ ID NO 688; 2081pp + Sequence Listing; English.
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             18-MAY-2001; 2001WO-US016450
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P-PSDB; ABB89717.
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cell proliferation; immunomodulatory; autoimmune disorder; antimicrobial; multiple sclerosis; rheumatoid arthritis; insulin-dependent diabetes; haematopoiesis; tissue growth activity; Parkinson's disease, cytostatic; Huntington's disease, Alzheimer's disease, chemotactic; chemokinetic; haemostatic; thrombolytic; tumour growth inhibitor; anabolic; contraceptive; autiinfertility; antiinflammatory; ss.
                                                             Human protein having hydrophobic domain encoding cDNA clone HP10784
                                                                                                                                                                                                  /product= "Human protein having hydrophobic domain"
/note= "CDS is specifically is claimed in claim 3"
                                                                               Human; hydrophobic domain; gene therapy; nutritional supplement;
                                                                                                                                                                        Location/Qualifiers
61. .849
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       standard; cDNA; 1461
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The present sequence is human protein with hydrophobic domain encoding cDNA clone HP10784. The polynucleotide and polypeptide of the invention may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate polypeptide expression. The polynucleotides continto a host cell and culturing the cell to express the protein. The polynucleotides and its complementary sequences may also be used as DNA probes in diagnostic assays and also used in gene therapy. The polypeptides may also be used as nutitional colypeptides may also be used as antigens in the production of antibodies and in assays to identify modulators of polypeptide expression and crivity. The polypeptides and nucleic acids may be used as nutritional supplements, to modulate cytokine and cell proliferation activity, to modulate immune stimulation or suppression (e.g. for the treatment of microbial infections and autoimmune disorders such as multiple sclerosis, rheumatopoiesis, to modulate tissue growth activity (e.g. for the haematopoiesis, to modulate tissue growth activity (e.g. for the treatment of Parkinson's disease, Huntington's disease and Alzhaimer's disease), to modulate activity and inhibin activity (e.g. for the fertility), to modulate chemotactic and chemokinetic activity, to modulate receptor modulate haemastacic and thrombolytic activity, to modulate receptor condulate inflammation and to inhibit tumour growth Human proteins with hydrophobic domains and the nucleic acids encoding them, useful for preventing diagnosing and treating e.g. cancer, Claim 4; Page 287-289; 563pp; English them, useful for preventing darkling darkling darkleimer's and inflammation.

WPI; 2001-418355/44. P-PSDB; AAE06579.

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The present invention relates to GLUTX proteins (AAF55865-AAF55871 and AAB66932-AAB66941). The GLUTX proteins are related to the facultative glucose carriers GLUTI-GLUTS and have hexose binding and/or transport function. The GLUTX proteins may be used in the diagnosis, prevention and treatment of hexose transport disorders such as ischaemia, diabetes, hyperglycaemia, hypoglycaemia, a glucose metabolism disorder and/or a neurodegenerative disease. The present sequence is the coding sequence
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                                                                                                                                     rAlaGlnProValAspAlaSerValGlyLeuAlaTrpLeuAlaValGlySerMetCysLe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rat; GLUTX; gene therapy; vaccine; hexose transport modulator; hexose transport disorder; ischaemia; diabetes; hyperglycaemia; ss; hypoglycaemia; glucose metabolism disorder; neurodegenerative disease.
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23-FEB-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2356 BP; 409 A; 786 C; 721 G; 440 T; 0 U; 0 Other;
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AACGTGCGGAGACAGAGTAGCCGAGTGTCGTGGGCGGAGGCCTGGGAGCCCCCGTGTGTAC 819
                        LysProPheIleIleGlyValSerLeuMetAlaPheGlnGlnLeuSerGlyValAsnAla 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          human; marker; expressed sequence tag; EST; arabidopsis; tumour;
stress-induced phenotype; hyperosmotic stress; colon cancer; immunogen;
                                                                                         940 GATGCAGCTATAGTTGGTGCTGTGAGGCTCCTGTCTGTGCTGATTGCCGCTGTCACCATG
                                                                                                                                                                                                                                                                                                                                                 1180 CTGATACCCCTGCTGCCCACCATGCTCTTCATTATGGGCTATGCCATGGGCTGGGGGCCC
                                                                         275 ValMetPheTyrAlaGluThrIlePheGluGluAlaLys---PheLysAspSerSerLeu
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                                                                                                                                                                                                                                                                                                                                   372 TrpLeuAlaValGlySerMetCysLeuPhelleAlaGlyPheAlaValGlyTrpGlyPro
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                                                                                                                           294 AlaSerValValValGlyValIleGlnValLeuPheThrAlaValAlaAlaLeuIleMet
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2356 227 78 164 17

Conservative: Mismatches:

958.50 59.22% 44.08% 39.01%

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GlyGlyValLeuGlyGlyTrpLeuValAspArgAlaGlyArgLysLeuSerLeuLeuLeu

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The invention relates to a novel method for determining if a nucleic acid is a marker for a predetermined phenotype/cell type of interest from a biological species. The method comprises performing a global comparison of a group of expressed sequence tags (ESTS) known to be expressed in the phenotype/cell type of interest with all ESTs expressed in normal tissue in order to identify ESTs that are preferentially expressed in the phenotype/cell of interest. A method of the invention is useful for determining whether a nucleic acid is a marker for a predetermined phenotype or cell type of interest from a biological species, preferably Arabidopsis or human. The cell type of interest is an abnormal cell such as a tumour cell, and the predetermined phenotype is a stress-induced phenotype such as hyperosmotic stress or high salt conditions. A method of the inventing is also useful for detecting a tumour cell, and for regulating or preventing the growth of a tumour cell. An antibody of the invention is useful for detecting a tumour cell, and for regulating or tumour-associated markers. A polypeptide of the invention is useful as an immunogen for vaccinating an animal. The present sequence encodes a tumour-associated markers. A polypeptide of the invention is useful as an immunogen for vaccinating an animal. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Determining if a nucleic acid is a marker for a phenotype/cell type of interest, by global comparison of expressed sequence tags known to be expressed in the phenotype/cell type with all ESTs expressed in normal
                                                                                                                                                                                                                                                       Krukovskaya LL;
                                                                                                                                                                                                                                                       Lobashev AV,
                                                                                                                                                                                                                                                             Kozlov AP,
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22-OCT-2001; 2001US-0330457P.
19-FEB-2002; 2002US-0357144P.
                                                                                                                                                                                                                                                             Yankovsky NK,
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P-PSDB; ADA84077.
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cancer;

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1433 CGCGGCCATCTGCTTGGTGAGCCTGGTGTTCACAGGCTGCTGTGTGCCCGAGACCAAGGG 1492
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     carrier type 2A; SLC2A; glucose transporter; p53;
                                                                            yLysThrLeuGluGlnIleThrAlaHisPheGlu---GlyArg 477
                                                                                                             ACGGTCCCTGGAGCAGATCGAGTCCTTCTTCCGCACGGGGAGA
                                                                                                                                                                                                                                                                                                                                                                                                   carrier type 2A nucleic acid 15489280.
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2002US-0357253P.
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10-OCT-2001;
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The present sequence is that of human solute carrier type 2A (SLC2A)

nucleic acids 15489280. Genetic screens were designed to identify

modifiers of the p53 pathway in Drosophila in which p53 was
coverexpressed. Human orthologues (polymucleotides and polypeptides) of
one such modifier were then identified, including nucleic acid 15489280.
SLC2As are glucose transporter proteins with sugar transporter domains.
SLC2A nucleic acids and polypeptides are attractive drug targets for the
treatment of pathologies associated with a defective p53 signalling
carbway, such as cancer. The invention provides in vitro and in vivo
methods of assessing SLC2A function. Modulation of an SLC2A or its
binding partners is useful for understanding the association of the p53
cathologies. SLC2A-modulating agents that act by inhibiting or enhancing
SLC2A expression, directly or indirectly, e.g. by affecting an SLC2A
function such as transport or binding activity, can be identified using
methods provided. Modulators include small molecules, nucleic acids,
antibodies, antisense oligonuclectides and phosphothicate morpholino 721 G; 440 T; 0 U; 0 Other;

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                 |-----GCAGCCATCGTTGGGGCCGTGCTGTCCGTGCTGATCGCCCCCC
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                                                                                                                      1083 GCCAACCTGACTCTGGGCTGTACATCCACTTT-----GGCCCCCAGGCCTCTGAGC
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                                                 312 IleMetAspArgAlaGlyArgArgLeuLeuValLeuSerGlyValValMetValPhe
                                                                                               SerThrSerAlaPheGlyAlaTyrPheLysLeuThrGlnGlyGlyProGlyAsnSerSer
                                                                                                                                                                                              AlaSerValGly---LeuAlaTrpLeuAlaValGlySerMetCysLeuPheIleAlaGly
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T, Koga
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S, Otsuki
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K, Kojima
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1 T, Nagai
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11-JAN-2000; 2000JP-00118774.
02-MAY-2000; 2000JP-00183765.
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P-PSDB; AAM93417.
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|GGAGGCCTGAGTGCCATGATCCTCAACGACCTCCTGGGCCGGAAGCTGATCCATGTTC
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227
78
164
47
                      Conservative:
Mismatches:
Indels:
                                                                                                        ProGlu---AspProGluGluThrGlnProLeuLeuGly
 Length:
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                                            The invention relates to primers for synthesising full length cDNA clones. 830 cDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have been determined. Primers for synthesising the full length cDNA are useful length clones were obtained by construction of full length cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA estimers methods. The present sequence is a full length human cDNA of the invention. Note: The sequence data for this patent did not form part of the primer bench as precipilation, but was obtained in CD-ROM format directly
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                                                                                         GTCCGGAGAGAGCAGCCGAGTATCGTGGGCTGAAGGCACGGGCCCCACACGTGTGCCGG
                                                                                                                                      ---AlaGluGlnSerPheHisLeu-----AlaLeuLeuArgGlnProGlyIleTyrLys
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|CCCATCACCGTGGCCTTGCTGATGCGCCTCCTGCAGCAGCTGACGGGCATCACGCCCATC
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366 AlaSerValGly---LeuAlaTrpLeuAlaValGlySerMetCysLeuPheIleAlaGly 384
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AACAAAAGGGTGTTCCTGGCCACCTTCGCCGCAGTGCTCGGCAATTTCAGGTATTTGGGTAT 199
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|GAGGCCTGAGTGCCATGATCCTCCAACGACCTCCTGGGCCGGAAGCTGAGCATGATGTTC
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nucleic acids 12735203 and 9938031. In the present invention, genetic
screens were designed to identify modifiers of the p53 pathway in
screens were designed to identify modifiers of the p53 pathway in
corosophila in which p53 was overexpressed. Human orthologues

(polynucleotides and polypeptides) of one such modifier were then
identified, including nucleic acids 12735203 and 9938031. SLC2As

clack including nucleic acids 12735203 and 9938031. SLC2As

nucleic acids and polypeptides are attractive drug targets for the
treatment of pathologies associated with a defective p53 signalling
pathway, such as cancer. The invention provides in vitro and in vivo
methods of assessing SLC2A function. Modulation of an SLC2A or its
binding partners is useful for understanding the association of the p53
cathologies. SLC2A-modulating agents that act by inhibiting or enhancing
SLC2A expression, directly or indirectly, ea, by affecting an SLC2A
function such as transport or binding activity, can be identified using
methods provided. Modulators include small molecules, nucleic acids,
antisoned.
                                                                                                                                                                                                                                                                                                                                                                                               Identifying candidate p53 pathway modulating agent as therapeutic target for disorders of defective p53 function e.g. cancer, by assaying purified solute carrier family 2 (SLC2A) polypeptide or nucleic acid with a test
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                                                                                    "Human SCL2A"
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                                     Location/Qualifiers
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10-OCT-2001; 2001US-0328605P.
15-FEB-2002; 2002US-0357253P.
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P-PSDB; ABP58363.
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Sequence 8, Appli Sequence 79, Appl Sequence 8, Appli Sequence 2378, App Sequence 45, Appl Sequence 45, Appl Sequence 25, Appl Sequence 9, Appli Sequence 27, Appl Sequence 11, Appl Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 21, Appli

Sequence 2, Applisequence 1198, App Sequence 1198, App Sequence 1, Applisequence 1, Applisequence 1, Applisequence 17, Applisequence 574, App Sequence 7, Appli

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Perfect score:

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Scoring table:

Minimum DB Maximum DB

Database :

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Sequence 4731, Application US/09489039A

Sequence 4731, Application US/09489039A

Patent No. 6610836

GENERAL INFORMATION:
APPLICANT: GATY BRECON et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPRESENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR APPLICATION NUMBER: US 60/117,747
SEQUENCE FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
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US-09-016-434-855

US-09-21-922-25

US-09-339-972-9

US-09-231-922-23

US-09-291-922-23

US-09-291-922-23

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US-09-291-922-21

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US-09-103-840A-2

US-09-291-922-1

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US-09-886-954A-1 (1-477) x US-09-489-039A-4731 (1-1545)

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Result No.

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PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
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                     GlnArgAlaAlaProProAlaProArgLeuAspAspAlaAlaAlaSerTrpPheGlyAla 74
                                                                   75 ValValThrLeuGlyAlaAlaAlaGlyGlyValLeuGlyGlyTrpLeuValAspArgAla
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Sequence 4762, Application US/09489039A
Patent No. 6610836
GENERAL INFORMATION:
APPLICANT: Gary Button et. al
APPLICANT: Gary Button et. al
TITLE OF INVENTION: WUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
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                                                                                                                                                                                                                                                                                               COMPUTE: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,655
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152
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                       ADDRESSEE: INCYTE PHARMACEUTICALS, INC. STREET: 3174 PORTER DRIVE
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                              GENERAL INFORMATION:
APPLICANT: Cocks, Benjamin G.
APPLICANT: Susan G. Stuart
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION
TITLE OF INVENTION: EXPRESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IELEFAX: (650) 855-0555
INFORMATION FOR SEQ ID NO: 1104:
SEQUENCE CHARACTERISTICS:
LENGTH: 3915 hard
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CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9.58e-49
570.50
49.90%
31.60%
23.22%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid_
STRANDEDNESS: single
                                                                                                                                                NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                           E: CALIFORNIA
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Best Local Similarity:
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US-09-023-655-1104
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|TCATCGTTTTCGCCATGAGCGCCGGCCCACTTTGGGTACTGTGCTCCGAAATC 1167
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                                                                                        549
                                                                                                                  TrpLeuAlaValLeuGlyCysValProProSerLeuMetLeuLeuLeuWetCysPheMet 202
                                                                                                                                            ProGluThrProArgPheLeuLeuThrGlnHisArgArgGlnGluAlaMetAlaAlaLeu 222
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                                                                  ---TCGCTGTTTAAAGACAACAGCAACTTCCGCCGCGCGGTGTTCCTCGGCATCCTGCTG
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                                        ValGlylje, eu LeuAjajyri, euAlaGlyTrpValLeuGlu-
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|CTGAAGGTAAAACAGTCCGGCTGG------
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US-09-023-655-1104
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96 ArgLysLeuSerLeuLeuLeuCysSerValProPheValAlaGly------PheAla 112

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527 157 584 177 544	; Sequence 17, Application US/09679686B ; Patent No. 6624343 ; GENERAL INFORMATION ; APPLICANT: Lightner, Jonathan E. ; APPLICANT: Lightner, Jonathan E. ; APPLICANT: Lightner, Jonathan E. ; APPLICANT: Rafaski, J. Antoni ; APPLICANT: Thorpe, Catherine J. ; TITLE OF INVENTION: HEXOSE CARRIER PROTEINS ; FILE REFERENCE: BB1160 US NA	LING DATE: 2003-01-16 ICATION NUMBER: 60/081,131 NG DATE: 1998-04-09 ICATION NUMBER: PCT/US99/07561 SEQ ID NOS: 24 Microsoft Office 97	Alignment Scores: 2.17e-46 Length: 1752 Alignment Scores: 2.17e-46 Matches: 150 Score: 542.50 Matches: 150 Percent Similarity: 47.50% Conservative: 88 Best Local Similarity: 29.94% Mismatches: 20.02 Query Match: 4 Caps: 14	US-09-886-954A-1 (1-477) x US-09-679-686B-17 (1-1752)  QY	52ProSerLeuGlnArgalaAlaProProAla	Db 276 GCCAGCCAGTACGACAACCAGCTGCTCCACCTCTAC 335  Qy 78 LeuGlyAlaAlaAlaGlyGlyValLeuGlyGlyTrpLeuValAspArgAlaGlyArgLys 97
Db 510 AGGCGCAATTCAATGCTAACCTGTTGGCTGCTCGCTGGTGGCTGCTTTATGGGA 569  113 ValileThralaalaGlnAspValTtpMetLeuLeuGlyGlyArgLeuLeuThrGlyLeu 132  113 ValileThralaaAgAGTGGTTGAATGCTGTTGGTGTTTTTGGCTC 629  Db 570 CTGTGTAAAGTGGTTGAATGCTGTTGATTGCTGTTTTTGGCTC 629  133 AlaCyGGlyVallaSerLeuValAlaProValTyrIleSerGluIleAlaTyrProAla 152  0y	690 CTGCGGGGTGCCTTTGGCACTCTCAACCAGCTGGGCATCGTTGTTGGAATTCTGGTGGCCTGTGGCCTGTGGCCTTGTGGGCATCGTTGGTGGCCTGGCCTGGCCTGGCCTGGCCTGGCCTTTTGTTTTTGTTCTGTTTTTGTTTTTT	207 ArgPheLeuLeuThrGlnHisArgArgGlnGluAlaMetAlaAlaLeuArgPheLeu 225  207 ArgPheLeuLeuThrGlnHisArgArgGlnGluAlaMetAlaAlaLeuArgPheLeu 225  207 ArgPheLeuLeuThrGlnHisArgArgGlnGluAlaMetAlaAlaLeuArgPheLeu 225  208 TrpGlyGerGluGlnGlyTrpGluAspProProIleGlyAlaGluGlnSerPheHis 244  226 TrpGlyGerGluGlnGlyTrpGluAspProProIleGlyAlaGluGlnSerPheHis 244  Db 930 TGGGGCACCCAGGATGTATCCCAAGACATCAGGAGATGAAAGATGCAAGGATG 989  Qy 245	DD 990 TCACAAGAAAGCACAGCGTGTAGAGCTTTTAGAGTGTCCAGCTACCGACAGCCC 1049  QY 257 PhelleIleGlyValSerLeuMetAlaPheGlnGlnLeuSerGlyValAsnAlaValMet 276  DD 1050 ATCATCATTTGTGTTCCAGCTCTCTAGAGCTCTTGGGATCATGTTC 1109  QY 277 PheTyralaGluThr1lePheGluGluAlaLy8PheLy8AspSerSerLeuAlaSerVal 296  Dh 1110 TATTAGCCAAAACATCATCAAGCAGGAGGTCAAAGCACATCTAGCCACATC 1169	297 1170 317 1230	37 37 13	Oy 377 SerMetCysLeuPhellealaGlyPheAlaValGlyTrpGlyProlleProTrpLeuLeu 396  337 SerMetCysLeuPhellealaGlyPheAlaValGlyTrpGlyProlleProTrpLeuLeu 396  337 MetSerGluilePheProLeuHisValLysGlyValAlaThrGlyIleCysValLeuThr 416  397 MetSerGluilePheProLeuHisValLysGlyValAlaThrGlyIleCysValLeuThr 416  398 MetSerGluilePheProLeuHisValLysGlyValAlaThrGlyIleCysValLeuThr 416  399 MetSerGluilePheProLeuHisValLysGlyValAlaThrGlyIleCysValLeuThr 416  390 MetSerGluilePheProLeuHisValLysGlyValAlaThrGlyIleuThr 416  390 MetSerGluilePheProLeuHisValLysGlyValAlaThrGlyIleuHeGraftGraftGraftGraftGraftGraftGraftGraft

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                                                                                                                                        APPLICANT: Allen, Stephen M.
APPLICANT: Lightner, Jonathan E.
APPLICANT: Rafalski, J. Antoni
APPLICANT: Thorpe, Catherine J.
TITLE OF INVENITON: HEXOSE CARRIER PROTEINS
FILE REFERENCE: BB1160 US NA
CURRENT APPLICATION NUMBER: US/09/679,686B
CURRENT FILING DATE: 2003-01-16
PRIOR APPLICATION NUMBER: 60/081,131
PRIOR FILING DATE: 1999-04-09
PRIOR FILING DATE: 1999-04-07
NUMBER OF SEQ ID NOS: 24
NUMBER OF SEQ ID NOS: 24
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                                                                                              ; Sequence 1, Application US/09679686B
; Patent No. 6624343
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FEATURE:
NAME/KEY: unsure
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ORGANISM: Zea mays
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OTHER INFORMATION:
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Best Local Similarity:
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SerLeuValAlaproValTyrIleSerGluIleAlaTyrProAlaValArgGlyLeuLeu 157
                                                                                      576 AACAICGGGTICCAGCTCAIGATCACCAICGGCAICCTGGCGGCGGCGCCTCAICAAITAC 635
                                                                                                                                   -AjagjyTrpValLeuGluTrpArgTrpLeuAlaValLeuGly 188
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                  636 GACACCAACAAGATCAAGGCCGGGTAC-----GGGTGGCGCATCAGCCTGGCCATCGCG
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                                                               GlySerCysValGlnLeuMetValValValGlyIleLeuLeuAlaTyrLeu-
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                                                                                                                                                                                             LeuAlaSerAlaPheCysIlePheSerValLeuPheThrLeuPheCysValProGluThr
383 AlaGlyPheAlaValGlyTrpGlyProlleProTrpLeuLeuMetSerGluIlePhePro
                                                              403 LeuHisValLysGlyValAlaThrGlyIleCysValLeuThrAsnTrpLeuMetAlaPhe
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Oy 286 AlaLysPheLysAspSerSerLeuAlaSerValValGlyValIleGlnVal 303	324		Qy 360 SerAlaGlnProValAspAlaSerValGlyLeuAlaTrpLeuAlaValGlySerMetCys 379	Qy 380 LeuPhelleAlaGlyPheAlaValGlyTrpGlyProlleProTrpLeuLeuMetSerGlu 399 ::::::::::::::	Qy 400 IlePheProLeuHisValLysGlyValAlaThrGlyIleCysValLeuThrAsnTrpLeu 419	Qy 420 MetAlaPheLeuValThrLysGluPheSerSerLeuMetGluValLeuArgProTyrGly 439	Qy 440 AlaPheTrpLeuAlaSerAlaPheCysIlePheSerValLeuPheThrLeuPheCysVal 459	Qy 460 ProGluThrLysGlyLysThrLeuGluGlnI1e 470	RESULT 7 US-09-643-597-135 ; Sequence 135, Application US/09643597 ; Patent No. 6426072	FORMATION: : Wang, Tongtong : Fan, Liqun : Kalos, Michael D.		CANT: CANT: CANT: CANT:		18-21 Ws Version	; ILBNOTH: 2856 ; TYPE: DNA ; ORGANISM: Homo sapien US-09-643-597-135	Alignment Scores: 3.76e-43 Length: 2856 Score: 514.50 Matches: 145
ment Scores:  No.: 518.00 it Similarity: 47.55\$ Match: 41.08\$		18 201	PhealaleuglyTyrSerSerProAlaIleProSerLeu :::	AGTAC	Oy 64LeudsphspalaalaalaserTrppheGlyalaValThrLeuGlyalaala 81		Qy 102 LeuCysSerValProPheValAlaGlyPheAlaValIleThrAlaAlaGlnAspValTrp 121	Oy 122 MetLeubeuGlyGlyArgbeuLeuThrGlyLeuAlaCysGlyValAlaSerLeuValAla 141	Qy 142 ProvaltyrIleSerGluIleAlaTyrProAlaValArgGlyLeuLeuGlySerCysVal 161	Oy 162 GlnLeuWetValValGlyIleLeuLeuAlaTyrLeuAlaGlyTrpValLeuGlu 180	Oy 181TrpArgTrpLeuAlaValLeuGlyCysValProProSerLeuMet 195	Qy 196 LeuLeuLeuMetCysPheMetProGluThrProArgPheLeuLeuThrGlnHisArg 214 ::: ::: ::: ::: :::	Qy 215 ArgGlnGluAlaMetAlaAlaLeuArgPheLeuTrpGlySerGluGlnGly 231	Oy 232 TrgGluAspProProlleGlyAlaGluGlnSerPheHisLeuAla 246 :::	Qy 247 LeuLeuArgGlnProGlyIleTyrLysProPheIleIleGlyValSerLeuWetAla 265	Oy 266 PheGlnGlnLeuSerGlyValAsnAlaValMetPheTyrAlaGluThrilePheGluGlu 285

Oy 398 SerGiulleReProceudisVallyGlyValalarhrolyIteCysValLeuThrAsn 417  Db 1353 GCTGAACTCTTCAGCAGGGTCCAGCTGCCAGCTTGCAGGTTCCAGGTTGCAGGTTCCAGGTTGCAGGTTCCAGGTTGCAGGTTCCAGGTTGCAGGTTCAGGTTCAGGTTCAGGTTCAGG	yalpheLeualaalaahealaalaalaLe gyalpheLeualaalaahealaalaalaLe  :::        ccrcargcrGGCrGrGGGAGGAGCAGTGCT	Qy         45 Gly
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Qy         418 TrpLeuMetAlaPheLeuValThrLysGluPheSerSerLeuMetGluValLeuArgpro 437           Db         1413 TGGACCTCAAATTCATGTGGCATGTGCTTCCAGTATGTGGAGCAACTGTGTGGTCCC 1472           Qy         438 TyrGlyAlaPheTrpLeuAlaSerAlaPheCysIlePheSerValLeu	RESULT 11 US-09-21-107-135 ; Sequence 135, Application US/09221107 ; Patent No. 6660838 ; GENERAL INFORMATION: ; APPLICANT: Wang, Tongtong ; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY OF LUNG CANCER ; TILE REPERENCE: 210121.455C2 ; CURRENT FILING DATE: 1998-12-22 ; NUMBER OF SEQ ID NOS: 161 ; SOFTWARE: PatentIn Ver. 2.0 ; SEQ ID NO 135 ; LENGTH: 2856 ; TYPE: DNA ; ORGANISM: Human US-09-221-107-135	Alignment Scores: Pred. No.: Pred. No.: 514.50 Matches: Score: Score: Pred. No.: 514.50 Matches: 145 Porcent Similarity: 4.92 Mismatches: 91 Mismatches: 168 Query Match: 4.0.94 Gaps: 145 Conservative: 91 Mismatches: 168 US-09-886-954A-1 (1-477) x US-09-221-107-135 (1-2856)  Qy 25 ArgValPheLeuAlaAlaAlaAlaAlaLeuGlyProLeuSerPheGlyPheAlaLeu 44	Qy         45 Gly	98   Valleudly
85 ValleuGly		2.7 orysercludinglypripolladpproprolledlyhladludingserpheHis 244  876 GGGACAGCTGACCTGACCTGACCTGAGGAGGAAGGAGGAGAGAGA		ProValSerAlaGlnProValA ::::: ACCATGGGGTAGGACTGGTGG MetCysLeuPhelleAlaGlyP :: ATCTTTGGGGTTTGTGGCGTTTTT SerGlullePheProLeuHisV :::   :::   GCTGAACTCTTCAGCGGGTC

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MetProGluThrProArgPheLeuLeuThrGlnHisArgArgGlnGluAlaMetAlaAla 221
                    RESULT 12
US-09-489-039A-4560
Sequence 4560, Application US/09489039A
Patent No. 6610836
                                                                                                                                                                               TYPE: DNA
ORGANISM: Klebsiella pneumoniae
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                                                                     GlyTrpValLeuGlu------------TrpArgTrpLeuAlaValLeu 187
                                                                                        GGC-----CTGGACTCCATCATGGGCAACAAGGACCTGTGGCCCCTGCTGCTGACCATC 755
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                                           Pheteuteu---ThrGlnHisArgArgGlnGluAlaMetAlaAlaLeuArgPheteuTrp
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                                                                                                                        CTGACCACACGCTTCGTGCCCATGTATGTGGGTGAAGTGTCACCCACACGCCTTTCGTGGG
                               LeuLeuGlySerCysValGlnLeuMetValValValGlyIleLeuLeuAlaTyrLeuAla
                                                                                                             GlyCysValProProSerLeuMetLeuLeuLeuMetCysPheMetProGluThrProArg
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ATATGTGCCATCCTGGCCTCCATGGCCTCTGTCATCCTTGGCTATGACATTGGGGTGATG 181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTCGTGGGCTCGTTGCTCATGGGTTTCGCCGTCAACTACGGCATGCTCATGGCGGCCGC 409
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                                                                                                                                                                                                                                                                              SerProAlaIleProSerLeuGlnArgAlaAlaProProAlaProArgLeuAspAspAla 67
                                                                                                                                                                                                                                                                                                                                                       230 CAGCTGGAGATCCTGATCGGGATCCTCAGTCTAGCTTCGCTGGC
                                                                                                                                                                                                                                                                                                                                                                                              GlyTrpLeuValAspArgAlaGlyArgLysLeuSerLeuLeuLeuCysSerValProPhe
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       LENGTH: 1914
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                                                                                               236 ProlleGlyAlaGluGin-SerPheHisLeuAlaLeuLeuArgGlnProGlyIleTyrLy 255
                                                                                                                                                                          GATTGTGATCATTGGCATGGTGCTCGCCATATTCCAGCAGTGGTGTGGGATTAACGTCAT 926
                                                                                                                                                                                                                                                                        aSerValVal----ValGlyValIleGlnValLeuPheThrAlaValAlaAlaLeuIleMe 313
                                                                                                                                                                                                                                                                                                                                tAspArgAlaGlyArgArgLeuLeuLeuValLeu----SerGlyValValMetValPh 331
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                                                                                                                             congrammaganamacamamagneneeragagagachangaercoccagangamace 866
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GTCCCCGAGTCGCCGCGCTGGCTCATGAAGGCCGGTAAACCGGAGCGCGCCCGGGCTGCG
                                                                                                                                                        255 sProPhellelleGlyValSerLeuMetAlaPheGlnGlnLeuSerGlyValAsnAlaVa
                                                                                                                                                                                                               275 lMetPheTyrAlaGluThrIlePheGluGluAlaLysPheLys---AspSerSerLeuAl
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Patent No. 6383776;
GENERAL INFORMATION:
APPLICANT: Allen, Sieve
APPLICANT: Hitz, Bill
APPLICANT: Tingey, Tony
APPLICANT: Tingey, Scott
TILE OF INVENTION: Plant Sugar Transport Proteins;
FILE REFERENCE: BB-1163
CURRENT FILING DATE: 1999-04-14;
EARLIER FILING DATE: 1999-04-14;
MUMBER: OF SEQ ID NOS: 30;
SOFTWARE: Microsoft Office 97;
SEQ ID NO 19
                                           LeuArgPheLeuTrpGlySerGluGlnGlyTrpGluAspPro
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1914 137 91 182 83

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649 220 709 223 769 229 829 243

263

---PheLeuTrpGlySerGlu

Query Match:         20.31%         Indels:         84           DB:         4         Gaps:         15           US-09-886-954A-1 (1-477) x US-09-591-025-8 (1-2592)         (1-2592)           Qy         9 ThxGlnProLeuLeuGlyProProGlyGlySerAlaProArgGlyArgArgValPheLeu 28	49 ProAlaileProSerLeuGinArghlaAlaProProAlaProArgLeuAspAspAlaAla	628 109 676		Oy 166 ValValGlyIleLeuLeuAlaTyrLeuAlaGlyTrpValLeuGlu 180	198 LeumetCysPheWetProGluthrProArgheLeuLeuThrGliHisargArgGln 21 198 LeumetCysPheWetProGluthrProArgheLeuLeuThrGliHisargArgGln 21 1970 CTGCTGCCCTTCCCGAGGCCCCCGCTACTTACATCATCAAAATCTCCAGGGG 10 217 GluAlaMetAlaLeuArgPheLeuTrpGlySerGluGlnGly 23 119	Qy 232TrpGluAspProProlleGlyAlaGluGlnSerPheHisLeuAlaLeuLeuArgGln 250	268 1210 288	
CACTTCTTCCAGCAGCACCAGCAACTCCGTCCAGTACAGCGCCCGCC	Db 1100 cTGCTGATCAGCACGGGGATGATTGTCTCGCTCATCTGCCTCCGGTCG 1153  Qy 341 LysLeuThrGlnGlyGlyProGlyAsnSerSerHisValAlaIleSerAlaProValSer 360  Db 1154GGGCTCACCGTCGCG 1168  Qy 361 AlaGlnProValAspAlaSerValGlyLeuAlaTrpLeuAlaValGlySer 377  Db 1169 GGGCATCACCGGACACCAAGGTCGCGTGGGCCGTCGCGTCG	378 MetCysLeuPheIleAlaGlyPheAlaValGlyTrpGlyProIleProTrpLeuLeuMet 1223 ACCTGTCTTCTTCTCTCGGCCTCGGGCCATCAGGGGGGGG	Qy 418 TrpLeuMetAlaPheLeuValThrLysGluPheSerSerLeuMetGluValLeuArgPro 437  1343 CGCTCACCAGCGTCATCTCCAGACACTCTCTCCAACCATCACCATC 1402  Qy 438 TyrGlyAlaPheTrpLeuAlaSerAlaPheCysIlePheSerValLeuPheThrLeuPhe 457  Db 1403 GGCGGCAGCTCTTACTCCAGCATCGCCGCGCTCGTTTCTTCACG 1462	Qy         458 CysValProGluThrLysGlyLysThrLeuGluGlnIle 470           Db         1463 TGCCTCCCGGAGACACGCGGCCGGACGCTGGAGGAGATG 1501           RESULT 14         1463 TGCCTCCCGAGACACGCGGACGCTGGAGGAGATG 1501	pplication US/09591025 03373 MATION: Bogan, Jonathan S. Lodish, Harvey F. ENTION: Method of Measuring ENTION: Targeting of GUUT4	; CURRENT APPLICATION NUMBER: US/09/591,025 ; CURRENT FILING DATE: 2000-66-09 ; PRIOR APPLICATION NUMBER: 1999-09-15 ; PRIOR PILING DATE: 1999-09-15 ; PRIOR FILING DATE: 1999-66-09 ; NUMBER: OF SEQ ID NOS: Version 4.0	8 A A: Artificial Sequence FORMATION: modified GLUT4 conta 5-8	Alignment Scores: 1.31e-41 Length: 2592  Pred. No.: 499.00 Matches: 155  Percent Similarity: 48.07% Conservative: 82  Best Local Similarity: 31.44% Mismatches: 173

Qy 43 AlaLeuGlyTyr	Qy 47SerSerProAla 50       ::	Qy 51 IleProSerLeuGlnArgAlaAlaProProAlaProArgLeuAspAsp 66 :::		0 4		Qy 114 IleThralaalaGlnAspValTrpMetLeuLeuGlyGlyArgLeuLeuThrGlyLeuAla 133	Qy 134 CysGlyValAlaSerLeuValAlaProValTyrIleSerGluIleAlaTyrProAlaVal 153		Qy 174 LeualadlyTrpValLeuGluTrpArgTrpLeuAla 185 :::	Qy 186 ValleuGlyCysValProProSerLeuMetLeuLeuLeuMetCysPheMetProGluThr 205	Oy 206 ProArgPheLeuLeuThrGlnHisArgArgGlnGluAlaMetAlaAlaLeuArgPhe 224	Oy 225 LeuTrpGlySerGluGlnGlyTrpGluAspProPro 236	Oy 237 IleGlyAlaGluGlnSerPheHisLeuAlaLeuLeuArgGlnProGlyIleTyrLys 255 :::	Oy 256 ProPhellelleGlyValSerLeuMetAlaPheGlnGlnLeuSerGlyValAsnAlaVal 275	276 1005	Qy 296 ValValValGlyValIleGlnValLeuPheThrAlaValAlaAlaLeuIleMetAspArg 315 :::		Oy 334 SerAlaPheGlyAlaTyrPheLysLeuThrGlnGlyGlyProGlyAsnSerSerHisVal 353
Qy 328 ValMetValPheSerThrSerAlaPheGlyAlaTyrPheLysLeuThrGlnGlyGlyPro 347	Qy 348 GlyAsnSerSerHisValAlaileSerAlaProValSerAlaGlnProValAspAlaSer 367  Db 1387 GCGGGCAIGTGGCTGTGCCATCCTGATGACTGTGGCTCTGCTGCTGGAGCGAGTT 1446	Oy 368 ValGlyLeuAlaTrpLeuAlaValGlySerMetCysLeuPheIleAlaGlyPheAlaVal 387	Qy 388 GlyTrpGlyProlleProTrpLeuLeuMetSerGlullePheProLeuHisValLysGly 407	Oy 408 ValAlaThrGlyIleCysValLeuThrAsnTrpLeuMetAlaPheLeuValThrLysGlu 427	Oy 428 PheSerSerLeuMetGluValLeuArgProTyrGlyAlaPheTrpLeuAlaSerAlaPhe 447	Qy 448 CysllePheSerValLeu	Qy 462 ThrLysGlyLysThrLeuGluGlnIleThralaHisPhe 474	RESULT 15 US-09-919-172-79 ; Sequence 79, Application US/09919172 ; Patent No. 6671545	; GENERAL INFORMATION: ; APPLICANT: Faris, Mary ; APPLICANT: Turner. Christopher M. ; TITHE OF INVENTION: PROGRAME CANCED MARKEDS	FILE REFERENCE: PA-0036 US CURRENT APPLICATION NUMBER: US/09/919,172 CURRENT FILING DATE: 2001-07-30 PRIOR APPLICATION NUMBER: 60/222 469	; PRIOR FILING DATE: 2000-07-28 ; NUMBER OF SEQ ID NOS: 102 ; SOFWARRE: PERL PROGRAM : SEO ID NO 79		D No. (	OTHER INFORMATION: a, t, c, g, or other 3-09-919-172-79	Alignment Scores:  Pred. No.:  Score:  Score:  Percent Similarity:  Best Local Similarity:  A 5.99	20.27% Indels:	US-US-886-954A-1 (1-477) x US-09-919-172-79 (1-5227) QY 23 GlyArgArgValPheLeuAlaAlaPheAlaAlaAlaAlaLeuGlyProLeuSerPheGlyPhe 42	

3TGT 1175	4 AlaileSerAlaProvalSerAlaGlnProvalAsp-AlaSerValGlyLeuAlaTrp-L 373		euAlaValGlySerMetCysLe		roTrpLeu	6 CCTGGTTCATGGTGGCTGAGTTTTTCAGTCAAGGACCACGTCCTGCTGCTGCTTAGCAATAG 1355	3 ysValLeuThrAsnTrpLeuMetAlaPheLeuValThrLysGluPheSerSerLeuMetG 433	1356 CTGCATTCAGCAATTGGACCTGCAATTTCATTGTAGCTCTGTGTTTCCAGTACATTGCGG 1415	3 luValLeuArgProTyrGlyAlaPheTrpLeuAlaSerAlaPheCysIlePheSerValL 453	6 ACTICTGIGGACCTIAIGTGITTTICCTCTTIGCTGGAGTGCTCCTGGCCTTTACCC 1472	3 euPheThrLeuPheCysValProGluThrLysGlyLysThrLeuGluGlnIleThrAlaH 473	IGITTACATTTTTAAAGTTCCAGAAACCAAAGGAAAGTCTTTTC	3 isPheGlu 475	1533 AATTCCAA 1540
1173	354 A	1176 Ġ	373 eı	1236 T	393 r	1296 CC	413 Y	1356 C	433 li	1416 A	453 el	1473 T	473 i	1533 A
qa	δλ	qq	<i>‰</i>	qa	λõ	qq	λō	qq	ò	qa	λō	qq	λō.	qq

Search completed: September 28, 2004, 04:18:30 Job time : 152 secs